SUBSTITUTE SPECIFICATION

PERIPHERAL BLOOD CELL MARKERS USEFUL FOR DIAGNOSING MULTIPLE SCLEROSIS AND METHODS AND KITS UTILIZING SAME

FIELD AND BACKGROUND OF THE INVENTION

The present invention relates generally to the field of diagnosis, treatment assessment and prognosis. More specifically, the present invention relates to peripheral blood cell expressed markers and kits and methods utilizing same for diagnosing, treating and assessing the state of multiple sclerosis (MS) in an individual. The present invention also provides cellular markers which are useful in distinguishing between different clinical courses of MS e.g.: probable, relapsing-remitting, secondary progressive or primary progressive as well as response to the therapy.

Multiple sclerosis is an autoimmune neurodegenerative disease, which is marked by inflammation within the central nervous system with lymphocyte attack against myelin produced by oligodendrocytes, plaque formation and demyelization with destruction of the myelin sheath of axons in the brain and spinal cord, leading to significant neurological disability over time. The disease frequently occurs in young adults between 20-40 years of age, is more prevalent in females than males (2:1), and has a characteristic geographical distribution – estimated prevalence in USA 120/100,000, (250,000 to 350,000 cases).

The annual cost of MS in USA was estimated about $34,000 per person, $2.2 million total lifetime cost per case or $6.8 billion yearly, in a conservative estimate of a national annual cost (Anderson DW, 1992; Whetten-Goldstain K., 1998).

Clinical Diagnosis and Evaluation of Stages of MS

Typically, at onset an otherwise healthy person presents with the acute or sub acute onset of neurological symptomatology (attack) manifested by unilateral loss of vision, vertigo, ataxia, dyscoordination, gait difficulties, sensory impairment characterized by paresthesia, dysesthesia, sensory loss,

urinary disturbances until incontinence, diplopia, dysarthria or various degrees of motor weakness until paralysis. The symptoms are usually painless, remain for several days to a few weeks, and then partially or completely resolve. After a period of remission, a second attack will occur. During this period after the first attack, the patient is defined to suffer from probable MS. Probable MS patients may remain undiagnosed for years. When the second attack occurs the diagnosis of clinically definite MS (CDMS) is made (Poser criteria 1983; C.M. Poser et al., Ann. Neurol. 1983;13, 227).

The clinical disease courses of MS are relapsing-remitting, primary or secondary progressive (Abramsky, 1997; Russell, 1998).

The relapsing-remitting course of MS (85% of patients) is characterized by acute attacks or relapses during which new neurological symptoms and signs appear, or worsen. Relapse develops within a period of several days, lasts for 6-8 weeks, than gradually resolves. During the acute relapse scattered inflammatory and demyelinating central nervous system (CNS) lesions produce varying combinations of motor, sensory, coordination, visual, and cognitive impairments, as well as symptoms of fatigue and urinary tract dysfunction. The outcome of a relapse is unpredictable in terms of neurological sequel but it is well established that with additional relapses, the probability of complete clinical remission decreases and neurological disability and handicap may develop. On average, about 60% of patients remain fully functional 10 years after the primary attack, and 25 to 30% remain fully functional 30 years after onset. Statistically, the disease does not greatly decrease life expectancy (mean decrease 12 years), although some patients become severely disabled and die from recurrent infections and complications.

Primary progressive MS (10% of patients) is characterized by slow, progressive neurological dysfunction usually in the form of a gradual myelopathy causing spasticity and ataxia. Treatment regimen varies greatly with different clinical course and severity of the disease.

The diagnosis of MS is still defined primary by clinical terms and relies on a combination of history, neurological examination and ancillary laboratory and neuro-imaging studies.

Laboratory tests for MS include: 1) CSF evaluation of IgG synthesis, oligoclonal bands; 2) MRI of the brain and spinal cord and; 3) exclusion of other autoimmune diseases by blood tests [e.g.,; serum B12 level; HTLV 1 or HIV 1 titers; sedimentation rate or C-reactive protein; RA latex (Rheumatoid arthritis); ANA, anti-DNA antibodies (systemic lupus erythematosus)]. However, accurate diagnosis and prognosis in the "probable" stage, and early relapsing-remitting stages remains problematic. For example, it has been shown that positive MRI findings in the first demyelinating attack only provide a 50% successful prediction of development of clinically definite MS within 2-3 years (CHAMPS Study Group, Neurology 2002;59:998-1005). Likewise, Villar et al (Neurology 2002;59:877-83) found that detection of oligoclonal IgM bands with early symptoms were only partially predictive of development of clinically definite MS.

Other laboratory tests may provide some additional support for the diagnosis, but evidence of lesions disseminated in time and space remains a cardinal element of the diagnosis (Poser CM., 2001). In absence of definitive laboratory tests and pathognomonic clinical features, MS remains ultimately a diagnosis of exclusion.

Diseases that may be confused with MS are: 1) Acute disseminated encephalomyelitis (follows infections or vaccination mainly in children, fever, headaches, and meningitis common), 2) Lyme disease (antibodies to Borrelia species antigens in serum and CSF), 3) HIV associated myelopathy (HIV antibodies present), 4) HTLVI myelopathy (HTLVI antibodies present in serum/CSF), 5) Neurosyphilis (syphilis antibodies present in serum and/or CSF, 6) Progressive multifocal leukoencephalopathy (biopsy of lesions demonstrates virus by electron microscopy), 7) Systemic lupus erythematosus (CNS

manifestations of lupus, antinuclear antibodies, anti-dsDNA), 8) Polyarteritis nodosa (systemic signs, micro-aneurysms demonstrated by angiographies, vasculitis demonstrated in biopsy of involved areas), 9) Sjogren's syndrome (dry eyes and mouth, antiRo and antiLa antibodies), 10) Behcet's disease (Oral/genital ulcers, antibodies to oral mucosa), 11) Sarcoidosis (CNS signs, increased protein in CSF, biopsy shows granuloma, 12) Paraneoplastic syndromes (older age group, antiYo antibodies), 13) Subacute combined degeneration of cord (peripheral neuropathy, vitamin B12 levels), 14) Sub acute myeloopticoneuropathy (adverse reaction to chlorhydroxyquinoline, mainly in Japanese), 15) Hereditary spastic paraparesis/ primary lateral sclerosis (normal CSF, MRI and visual evoked potential studies), 16) Adrenomyeloneuropathy (adrenal dysfunction, neuropathy, increased plasma very long-chain fatty acids), 16) Spinocerebellar syndromes (familial, pes cavus scoliosis, abnormal reflexes, normal CSF IgG), 17) Miscellaneous – strokes, tumors, arteriovenous malformations, arachnoid cysts, Arnold-Chiari malformations, and cervical spondylosis all may lead to diagnostic dilemmas on occasion. Thus, detailed history and neurological examination must be complemented by specific laboratory tests for the correct diagnosis of MS. Clearly there is a long felt need for more powerful diagnostic tools for prediction and staging of MS.

Etiology of MS

The etiology of MS is unknown. It is suggested that a combination of genetic background and environmental factors and immune response are involved in the disease. A certain incidence of familial occurrence has been observed, with the concordance rate among monozygotic twins being 30%, a 10-fold increase over that in dizygotic twins or first-degree relatives (Steinman, 1966; Dyment et al Mol. Gen 1997;6:1693-98). In addition, recent research indicates that the tissue damage in MS occurs as the result of pathological autoimmune responses to several myelin antigens following exposure to an as yet undefined environmental causal agent.

However, although some environmental factors have been statistically associated with the disease, none have provided correlations of any predictive value. Environmental factors seem to trigger MS in subjects who are already genetically susceptible to the illness. Most probably no one dominant gene determines genetic susceptibility, but rather many genes, each with different influence, are involved. Indeed, the initial pathogenic process could be caused by one group of genes, while others groups could be responsible for the development and progression of the disease (Oksenberg, 2001; Compston, 1997).

Microarray Analysis and MS

Microarray technology is based on hybridization of mRNA to high-density array of immobilized target sequences. Each sequence corresponds to a specific gene(s) of interest. The labeled pool of sample mRNA is subsequently hybridized to the array (chip). Application of this technology provides the capability of monitoring thousands of various genes simultaneously. Today commercial available DNA microarrays (Affymetrix, Santa Clara CA, USA) contain elements representing 10,000, 20,000 or more genes that have been characterized in terms of function or disease association. The preparation and use of microarrays for diagnostics, research and drug development is disclosed in, inter alia, US Pat. Nos. 6,324,497 and 6,468,476 to Friend et al and 6,410,229 to Lockhart et al; and Intnl Pat. Application WO 0053625C2 and A2.

Several application of microarrays in human disease have been reported, for example the identification (marker) genes involved in ovarian carcinogenesis (Ono K., 2000); classification of genes expression profiling of cutaneous malignant melanoma (Bitter M., 2000); and expression profile of Tangl-Rearing CA1 neurons in Alzheimer's disease (Stephen, 2000). Alizaden (2000) characterized gene expression in diffuse large B cell lymphoma, where two distinct gene expression patterns, characterized by different molecular forms of B cells lymphoma, were identified. In addition, microarray

technology has also been applied to diagnosis and monitoring of such diverse diseases as cancer (US Pat. No. 6,511,849 to Freuhauf et al), psoriasis (Intnl Pat. Application WO 20020027538 to Trepicchio et al), T-helper cell related diseases (Trepicchio et al , Intnl Pat Application WO 20020039734), Epstein-Barr disease (U.S. Pat. Nos. 6,506,553 and 6,468,476 to Smith and Parks), rheumatoid arthritis (Intnl Pat Application WO 0248310A2 to Trepicchio et al) and Reward Deficiency Syndrome, all of which are incorporated herein by reference.

In a recent review (Greenberg SA., 2001) the author discussed the potential application of DNA microarray technology for understanding neurological disorders. Using cDNA microarrays technology, brain tissue from pathology lesions and normal white matter of single MS patient were analyzed (Whitney LW.,1999). Blood genomic fingerprints were demonstrated after experimental strokes, seizures, hypoglycemia and hypoxia of rats (Yang Tang, 2001). Similarly, microarray analysis of gene expression in brainstem and spinal cord tissues from the animal models of MS (experimental autoimmune encephalomyelitis, EAE) has identified a number of differentially expressed genes from active-acute versus silent lesions (Lock C. et al Nat Med 2002;8,500-504), and also suggested a role for the proinflammatory cytokine osteopontin in the development of EAE in mice (Chabas D et al Science 2001;294:1731-34).

In another recent study, Ramanathan M et al (J of Immunology 2001;116:213-19) used cDNA microarray technology to identify abnormal gene expression patterns in PBMC of relapsing-remitting MS patients. The study compared PBMC gene expression in 15 patients during remission (only) with that of 15 healthy controls, using a GeneFilters GF211 array (Research Genetics, Huntsville AL, USA) having approximately 5200 human gene sequences. Groups of marker genes correlated with MS were disclosed, but the range of differences (fold changes) between level of gene expression in MS and

control groups was only 13 to 35 % for unregulated and from 11 to 43% for down regulated genes. Such small differences are probably due to the limited sensitivity of the technology employed in using GeneFilters arrays, and may not have any clinical or diagnostically mining significance. More significantly, the population of MS patients was limited, including only patients during clinical remission, who had not received any immunosupressive treatment for at least 3 months. Thus, the markers described do not provide a profile of expression patterns useful for diagnosing clinically defined MS in patients having probable MS, or for determining stages of the disease.

Trepicchio et al. (Intnl Pat. Application No. WO 02/079218 A1) also describe the use of microarray technology in determining characteristic gene expression in an animal model of MS (murine EAE) and in tissue samples from MS patients. The human samples were PBMC or brainstem tissue, collected from 60 patients manifesting a wide variety of symptoms, at different stages of MS including relapsing-remitting, primary and secondary progressive, and acute exacerbation. RNA probes prepared from these samples were hybridized to a human chip array containing approximately 14,000 gene sequences (MicroArray, Affymetrix, cat no. 510448, Santa Clara CA), and expression profiles compared with those of healthy controls. Determination of the panel of "MS-related" markers was based merely on fold change of greater than 2 fold (up- or downregulated), with a confidence level of $p<0.01$. No more stringent statistical criteria were applied. A "panel" of 300 differentially regulated genes was thus described in the PBMC samples, and another 100 in the brain lesion tissue. However, no classification of expression profiles characteristic to specific stages of the disease was provided, and the "class predictor model", as described, using "neighborhood analysis", was applied for attempted prediction of "MS-afflicted" or "non-diseased" samples only. Thus, the panel of markers described is not applicable to the diagnosis of stage of MS, in general, is

unsuited for the prediction of clinically definite MS or probable MS patients, and is clearly non-predictive in monitoring response to treatment.

There is thus a widely recognized need for, and it would be highly advantageous to have gene expression profiles useful in distinguishing between different forms of MS e.g.: probable, relapsing-remitting, primary or secondary as well as response to the therapy, devoid of the above limitations.

SUMMARY OF THE INVENTION

According to one aspect of the present invention there is provided a method of diagnosing a subject with multiple sclerosis, the method comprising determining a level of expression of at least one gene selected from the group consisting of the genes listed in Tables I-V in a sample obtained from the subject, wherein a substantial difference between the level of expression of the gene in the sample obtained from the subject and a normal expression level of the gene is an indication that the subject is afflicted with multiple sclerosis.

According to further features in preferred embodiments of the invention described below a method of monitoring a state of multiple sclerosis in a subject, the method comprising monitoring a level of expression of at least one gene selected from the group consisting of the genes listed in Tables I-V over a predetermined time period, wherein substantial difference between the levels of expression of the at least one gene over the predetermined time period indicates a change in a state of the multiple sclerosis in the subject.

According to further features in preferred embodiments of the invention described below monitoring the level of expression of at least one gene over the predetermined time period is effected by periodically obtaining a sample from the individual and determining the level of expression of the at least one gene in the sample.

According to still further features in the described preferred embodiments the at least one gene comprises at least 10, at least 50, at least 100, at least 250, at least 500, at least 750, at least 1000 or at least 1200 genes

each independently selected from the group consisting of the genes listed in Tables I-V.

According to another aspect of the present invention there is provided a method of diagnosing a subject with multiple sclerosis, the method comprising the step of determining a level of expression of each of the genes listed in Tables I-V in a sample obtained from the subject, wherein a substantial difference between expression levels of the genes in the sample obtained from the subject and normal expression levels of the genes is an indication that the subject is afflicted with multiple sclerosis.

According to further features in preferred embodiments of the invention described below the normal expression level of the at least one gene or genes is determined by measuring the level of expression of the gene or genes in at least one control sample obtained from at least one healthy individual.

According to still further features in the described preferred embodiments the sample includes peripheral blood mononuclear cells.

According to yet further features in the described preferred embodiments the substantial difference is a difference statistically significant at a confidence level of p= 0.05 as determined by at least one test selected from the group consisting of a t-test, a TNoM and an INFO score.

According to further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes is determined by quantifying a level of a protein product thereof in the sample.

According to still further features in the described preferred embodiments quantifying a level of the protein is effected using a reagent which specifically binds with the protein.

According to yet further features in preferred embodiments of the invention described below the reagent comprises an antibody or fragments thereof.

According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table I.

According to still further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table II.

According to yet further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table III.

According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table IV.

According to still further features in the described preferred embodiments at least one gene or genes are selected from the genes listed in Table V.

According to yet further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes in the sample is determined by detecting the presence in the sample of a transcribed polynucleotide or portion thereof. The transcribed polynucleotide can be mRNA.

According to further features in preferred embodiments of the invention described below the transcribed polynucleotide or portion thereof is detected via a labeled probe which specifically hybridizes with the transcribed polynucleotide or portion thereof.

According to still further features in the described preferred embodiments the sample from a subject is T cells, the at least one gene or genes are selected from the genes listed in Table IV and the normal expression of the gene or genes is T-cell expression.

According to an additional aspect of the present invention there is provided a method of assessing the efficacy of a treatment regimen on multiple sclerosis in a subject, the method comprising determining a level of expression of at least one gene or genes selected from the group consisting of the genes listed in Tables I-V in samples obtained from the subject prior to, and following exposure to the treatment regimen, wherein a substantial difference in the expression level of at least one gene or genes between the samples is an indication that the treatment regimen is efficacious in treating multiple sclerosis in the subject.

According to further features in preferred embodiments of the invention described below the treatment regimen is administering at least one test compound for inhibiting multiple sclerosis.

According to still further features in the described preferred embodiments the treatment regimen is an environmental condition.

According to yet further features in the described preferred embodiments the substantial difference is a difference statistically significant at a confidence level of $p= 0.05$ as determined by at least one test selected from the group consisting of a t-test, a TNoM and an INFO score.

According to further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes is determined by quantifying a level of a protein product thereof in the sample.

According to still further features in the described preferred embodiments quantifying a level of the protein is effected using a reagent which specifically binds with the protein.

According to yet further features in preferred embodiments of the invention described below the reagent comprises an antibody or fragments thereof.

According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table I.

According to still further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table II.

According to yet further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table III.

According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table IV.

According to still further features in the described preferred embodiments at least one gene or genes are selected from the genes listed in Table V.

According to yet further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes in the sample is determined by detecting the presence in the sample of a transcribed polynucleotide or portion thereof. The transcribed polynucleotide can be mRNA.

According to further features in preferred embodiments of the invention described below the transcribed polynucleotide or portion thereof is detected via a labeled probe which specifically hybridizes with the transcribed polynucleotide or portion thereof.

According to still further features in the described preferred embodiments the sample from a subject is T cells, the at least one gene or genes are selected from the genes listed in Table IV and the normal expression of the gene or genes is T-cell expression.

According to still further features in the described preferred embodiments the at least one gene comprises at least 10, at least 50, at least 100, at least 250, at least 500, at least 750, at least 1000 or at least 1200 genes each independently selected from the group consisting of the genes listed in Tables I-V.

According to another aspect of the present invention there is provided a kit for diagnosing multiple sclerosis in a subject, the kit comprising components suitable for determining expression levels of at least one gene selected from the group of genes listed in Tables I-V.

According to further features in the described preferred embodiments the reagents include at least one polynucleotide sequence selected capable of specifically hybridizing with an transcription product of the at least one gene and reagents for detecting and optionally quantifying a complex formed from the at least one polynucleotide sequence and said transcription product.

According to still further features in the described preferred embodiments the reagents include at least one antibody selected capable of specifically binding a polypeptide product of the at least one gene and reagents for detecting and optionally quantifying a complex formed from the at least one antibody and the polypeptide product.

According to further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed in Table I.

According to still further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed in Table II.

According to yet further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed in Table III.

According to further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed in Table IV.

According to still further features in the described preferred embodiments at least one gene is selected from the genes listed in Table V.

According to further features in preferred embodiments of the invention described below the kit further comprises packaging material identifying the kit as useful from diagnosing MS.

According to another aspect of the present invention there is provided a polynucleotide array comprising at least 10 and no more than 1500 polynucleotide sequences, wherein each of the sequences is selected capable of hybridizing with a transcription product of a polynucleotide sequence of a gene selected from the group of genes listed in Tables I-V.

According to further features in preferred embodiments of the invention described below the array is selected having polynucleotide sequences capable of diagnosing subjects suspected of suffering from multiple sclerosis. The subjects may also be suspected of suffering from probable multiple sclerosis, primary progressive multiple sclerosis, secondary progressive multiple sclerosis, and/or relapsing/remitting multiple sclerosis.

According to further features in preferred embodiments of the invention described below the gene is selected from the genes listed in Table I, II, III, IV and/or IV.

According to yet another aspect of the present invention there is provided an array comprising at least 10 and no more than 1500 antibodies or antibody fragments each capable of specifically binding a protein product of a gene selected from the group of genes listed in Tables I-V.

According to further features in preferred embodiments of the invention described below the array is selected having antibodies or antibody fragments capable of diagnosing subjects suspected of suffering from multiple sclerosis.

The subjects may also be suspected of suffering from probable multiple sclerosis, primary progressive multiple sclerosis, secondary progressive multiple sclerosis, and/or relapsing/remitting multiple sclerosis.

According to further features in preferred embodiments of the invention described below the gene is selected from the genes listed in Table I, II, III, IV and/or IV.

Implementation of the method and system of the present invention involves performing or completing selected tasks or steps manually, automatically, or a combination thereof. Moreover, according to actual instrumentation and equipment of preferred embodiments of the method and system of the present invention, several selected steps could be implemented by hardware or by software on any operating system of any firmware or a combination thereof.

BRIEF DESCRIPTION OF THE DRAWINGS

The invention is herein described, by way of example only, with reference to the accompanying drawings. With specific reference now to the drawings in detail, it is stressed that the particulars shown are by way of example and for purposes of illustrative discussion of the preferred embodiments of the present invention only, and are presented in the cause of providing what is believed to be the most useful and readily understood description of the principles and conceptual aspects of the invention. In this regard, no attempt is made to show structural details of the invention in more detail than is necessary for a fundamental understanding of the invention, the description taken with the drawings making apparent to those skilled in the art how the several forms of the invention may be embodied in practice.

In the drawings:

FIGs. 1A-B are graphic representations of the differences in PMBC gene expression between MS patients and healthy subjects. RNA from Peripheral

Blood Mononuclear Cells (PMBC) of 26 patients diagnosed with MS, and 18 healthy, age-matched controls was purified, labeled hybridized to a Genechip array (U95Av2, Affymetrix Inc. Santa Clara CA, USA), scanned and analyzed according to manufacturer's recommendations. The data were normalized and fold ratios calculated for each gene of the MS samples against the geometric mean of the controls. Figure 1A shows the number of MS specific genes detected having increased expression (fold change greater than 1.5) analyzed by t-test (red line), TNoM (green line) and INFO (blue line), compared with random occurrence (black line), at confidence levels (False Discovery Rates, FDR) of 90% (p= 0.10) to 100% (p= 0). Note the high level of significant MS-related gene expression at 95% FDR and above (arrows) (1249 distinguished genes). Figure 1B is an infogram of the 1249 genes most significantly ($p<0.05$ on all three tests) distinguishing MS patients (MS) from (control) healthy controls, determined as above. Each spot represents expression of a specific gene; color intensity of overexpressed (green) and under-expressed (red) genes indicates fold increase as compared to controls. Gray color indicates genes showing no difference in expression between MS and controls.

FIGs. 2A-B are graphic representations of the differences in PMBC gene expression between MS patients during acute relapse, and MS patients in remission. RNA from PMBC of 12 relapsed, and 14 clinically in remission patients was purified, labeled, hybridized and analyzed as described for Figures 1A-B hereinabove. Figure 2A shows the number of acute relapse-specific genes detected having increased expression in relapse, as analyzed by t-test (red line), TNoM (green line) and INFO (blue line), compared with random occurrence (black line), at confidence levels (False Discovery Rates, FDR) of 90% (p= 0.10) to 100% (p= 0). 735 genes were detected having significant relapsing-related gene expression at 95% FDR and above. Figure 2B is an infogram analysis of the 735 genes most significantly ($p<0.05$ on all three tests) distinguishing acute relapsing MS patients (Relapse) from MS patients in

remission (Remission). Note the different profiles of gene expression in patients undergoing treatment (Relapse + and Remission +) compared with untreated patients (Relapse- and Remission -).

FIG. 3 is a pie chart diagram showing the breakdown, by functional character, of specific genes displaying up- or down-regulation in MS-derived MOG-reactive T-cell lines, as compared to normal-derived MOG-reactive T-cell lines. Significant MOG reactive MS-related genes are defined as genes with TNoM=0 and p=0.057 as compared to normal MOG-reactive T-cells.

FIG. 4 is a graphic representation of the differences in gene expression between MOG-stimulated T-cell lines from MS patients and healthy controls. RNA from MOG-stimulated T-cells of 4 MS patients and 3 matched controls was purified, labeled, hybridized and analyzed as described for Figures 1A-B hereinabove. Panel A shows a cluster analysis of 150 differentially expressed genes analyzed as described hereinabove (TNoM=0, $p<0.05$) distinguishing T-cells of MS (MS) patients from controls (Controls). Panel B shows a cluster analysis of the 43 most informative genes (TNoM=0, $p<0.05$, and fold change> 1.5). Each row represents a gene, and each column represents a T-cell line form a different subject. Yellow color indicates genes with an increased expression relative to controls are yellow, and blue color indicates genes with relative decreased expression.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention is of methods and kits for diagnosing multiple sclerosis in subjects, using novel gene expression profiles derived from peripheral blood cells. Specifically, the present invention can be used to diagnose MS in early stages of the disease, to determine clinical stage and predict the course of the disease in patients with a unclear diagnoses, to provide definition and prognostic information in patients with probable MS, to assess

and monitor MS therapies and to screen new and established drugs and treatments for MS.

The principles and operation of the present invention may be better understood with reference to the drawings and accompanying descriptions.

Before explaining at least one embodiment of the invention in detail, it is to be understood that the invention is not limited in its application to the details of construction and the arrangement of the components set forth in the following description or illustrated in the Examples and drawings. The invention is capable of other embodiments or of being practiced or carried out in various ways. Also, it is to be understood that the phraseology and terminology employed herein is for the purpose of description and should not be regarded as limiting.

The present invention provides previously unavailable accuracy in predicting and staging MS, by identifying genes and groups of genes specifically over- and under-expressed in PBMC of patients at various stages of their disease.

As is further described in the Examples section which follows, the present inventors have conducted a broad scale analysis of PMBC expressed genes using hybridization of biotin-labeled PBMC mRNA to more than 12,000 human gene sequences provided on DNA chips. By utilizing specialized statistical analysis approaches, the present inventors identified in the microarray data the most highly informative expression profiles.

As mentioned hereinabove, multiple sclerosis is a chronic, multi-factorial neurodegenerative disease of unknown etiology, the diagnosis and classification of which remains largely clinical in nature. Identification of the stages and progression of the disease, particularly definition of the probable MS stage, is crucial to determination of optimal treatment regimen and development of effective therapies. However, the complexities of autoimmune interactions, and the variability of MS in different individuals have made diagnosis and

subsequent prognosis using traditional methods inexact and challenging. Methods for more accurate diagnosis of MS are greatly needed.

The profiles of MS-related genetic markers listed in Table I represent genes exhibiting differential expression in PBMCs from a large sample of MS patients, compared to that of age-matched healthy controls. Abundance of specific gene transcripts, represented by the intensity of label hybridizing to individual sequence loci of the MicroArray (Affymetrix Inc, Santa Clara CA), was recorded and quantified according to the manufacturers recommended protocols (such as GeneChip 3.0 software from Affymetrix). However, rather than composing the profile of differentially expressed genes based on probabilities using simple distribution of mean intensities, as has been reported by Ramanathan et al (J Immunol 2001;116:213-219), informative genes were selected based on the degree to which they were predictive of classification of the sample as "diseased" or "not diseased". By applying the rigorous three-pronged statistical analysis described in detail hereinbelow, 1249 genes most informative in distinguishing between diseased and otherwise not diseased patients were identified (see Table I). By applying an even more restrictive analysis of the data in Table I (see Table II, Bonfferoni analysis), a subset of the 300 highest scoring genes was identified. These MS marker genes comprise both over-expressed and downregulated genes, and represent of a diverse group of functional gene categories. Additional analysis of the markers uncovered herein also led to the identification of another restricted marker set which can be accurately utilized to diagnose probable MS patients. As is further described hereinbelow, the identification of such a marker set represents a significant breakthrough since it enables to treat individuals at a much earlier stage of MS then previously possible.

Thus, according to one aspect of the present invention there is provided a method of diagnosing a subject with multiple sclerosis by determining a level of expression of at least one gene of the genes listed in Tables I-V in a sample

obtained from the subject, wherein a substantial difference between the level of expression of the gene in the sample obtained from the subject and a normal expression level of the gene is an indication that the subject is afflicted with multiple sclerosis.

Normal expression levels of a marker or markers are obtained from isolated or cultured PMBCs (e.g., T-cell cultures), or samples obtained from individuals not affected with MS. A substantial difference is preferably of a magnitude that is statistically significant (see the Examples section for more detail). In particularly preferred embodiments, the marker is increased or decreased relative to control samples by at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, or 10-fold or more. Similarly, one skilled in the art will be well aware of the fact that a preferred detection methodology is one in which the resulting detection values are above the minimum detection limit of the methodology utilized.

As is further described in the Examples section which follows, the marker listed in Tables I-V were identified in peripheral blood cells. As such, the sample obtained from the individual is preferably a peripheral blood sample or any sample which includes blood cells such as T-cells. In a preferred embodiment, the sample is blood, thymus, spleen, lymph, pus, or bone marrow. However, it will be apparent to one skilled in the art that PMBCs may be present as an infiltrate in many other tissues, and that such tissues may also serve as samples in which the presence, activity, and/or quantity of the markers of the invention may be assessed. The tissue samples containing one or more of the markers themselves may be useful in the methods of the invention, and one skilled in the art will be well aware of methods by which such samples may be conveniently obtained, stored, preserved and processed. For further description relating to collection and processing of blood samples please see the Examples section which follows.

As is detailed in the Examples section below, analysis of PBMC genes differentially expressed in MS, according to the methods described herein,

revealed groups of genes of specific interest in MS. Genes that are most significantly over expressed, or downregulated in MS can indicate members of pathways important to disease development or pathology. Strongly overexpressed genes, according to Tables I and II, include **SLAM** (signaling lymphocyte activation molecule, GenBank Accession No. U33017), **LEF1** (lymphoid enhancer-binding factor 1, GenBank Accession No. AL099409), **LRP5** (low density lipoprotein receptor-related protein 5, GenBank Accession No. AF077820), **LILRB** (leukocyte immunoglobulin-like receptor, GenBank Accession No. AF004230), **LY75** (lymphocyte antigen 75, GenBank Accession No. AF011333), **CDW52 (**GenBank Accession No. N90866), **PIP5K1-gamma** (Phosphatidylinositol-4-phosphate 5-kinase, type 1, gamma, GenBank Accession No. AB011161), **MAP4** (Microtubule-associated protein 4, GenBank Accession No. M64571), **CTSK** (Cathepsin K, GenBank Accession No. X82153) and **CTSB** (Cathepsin B, GenBank Accession No. L22507). Strongly down-regulated genes include **IL1B** (Interleukin 1 beta, GenBank Accession No. M15330), **TRAF6 (**GenBank Accession No. U78798), **SCYA20** (GenBank Accession No. U64197), **IL1R** (type1 receptor, GenBank Accession No. M27492), **IL1RAP** (receptor accessory protein, GenBank Accession No. AB006537) and **IL1RN** (receptor antagonist, GenBank Accession No. X52015), **TGFB1** (Transforming growth Factor beta 1, GenBank Accession No. X05839), **SKI** (v-ski sarcoma viral oncogene homologue, GenBank Accession No. X15218), **VEGF** (Vascular endothelial growth factor, GenBank Accession No. M63978), **IGFBP4** (Insulin-like growth factor binding protein 4, GenBank Accession No. U20982), **EREG** (epiregulin, GenBank Accession No. NM_001432.1), and **NR4A1, NR4A2, NR4A3** (nuclear receptor family genes, GenBank Accession Nos. NM_002135.1, X75918 and U12767, respectively).

Functional groups of genes strongly represented in the profile of most significantly differentially regulated genes in MS include, inter alia, apoptosis-

related genes, T-cell activation and expansion related genes, cell proliferation related genes and epidermal growth factor genes. Many of the marker genes identified are associated with other MS- related genes, according to Tables I-V.

It will be appreciated that although a single marker can be used for diagnosis, diagnostic accuracy typically increases with an increase in the number of markers utilized.

As such, the diagnostic method of the present invention preferably utilizes a marker set that can range anywhere from 2 genes to 1200 genes. For example, the present method can utilize at least 10, at least 50, at least 100, at least 250, at least 500, at least 750, at least 1000 or at least 1200 genes each independently selected from the group consisting of the genes listed in Tables I-V. Most preferably the markers utilized are selected from the sequences listed in Table II.

The markers sets utilized can be selected according to a statistical significance or fold change thereof (provided for each marker in Tables I-V), a higher significance and higher fold change indicating higher probability of marker accuracy. For example, a selected marker set can encompass markers displaying a high statistical significance (low P-value), preferably a P-value lower than 5.0E-02, more preferably lower than 5.0E-04, most preferably, lower than 5.0E-06. Alternatively, markers can be selected according to shared features of the marker gene. For example, gene markers of similar cellular function (e.g., genes of a signaling pathway such as apoptosis) or markers displaying similar activity (e.g., enzymes of the same enzyme family) can be grouped into specific marker sets.

Each marker set may be considered individually, although it is within the scope of the invention to provide combinations of two or more marker sets for use in the methods and compositions of the invention to increase the confidence of the analysis.

As used herein, the terms "polynucleotide" and "oligonucleotide" are used interchangeably, and include polymeric forms of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The following are non-limiting examples of polynucleotides: a gene or gene fragment, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component. The term also includes both double- and single-stranded molecules. Unless otherwise specified or required, any embodiment of this invention that is a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double-stranded form.

As used herein, a "gene" includes a polynucleotide containing at least one open reading frame that is capable of encoding a particular polypeptide or protein after being transcribed and translated. Any of the polynucleotide sequences described herein may be used to identify larger fragments or full-length coding sequences of the gene with which they are associated. Methods of isolating larger fragment sequences are known to those of skill in the art, some of which are described herein. A "gene product" includes an amino acid (e.g., peptide or polypeptide) generated when a gene is transcribed and translated.

As used herein, a "probe" is defined as an oligonucleotide that is provided as a reagent to detect a target present in a sample of interest by hybridizing with the target. Usually, a probe will comprise a label or a means by which a label can be attached, either before or subsequent to the hybridization reaction. Suitable labels include, but are not limited to radioisotopes, fluorochromes, chemiluminescent compounds, dyes, and proteins, including enzymes.

As used herein, "expression" includes the process by which polynucleotides are transcribed into mRNA and translated into peptides, polypeptides, or proteins. "Differentially expressed", as applied to a gene, includes the differential production of mRNA transcribed from a gene or a protein product encoded by the gene. A differentially expressed gene may be overexpressed or underexpressed as compared to the expression level of a normal or control cell. In one aspect, it includes a differential that is 2.5 times, preferably 5 times or preferably 10 times higher or lower than the expression level detected in a control sample. The term "differentially expressed" also includes nucleotide sequences in a cell or tissue which are expressed where silent in a control cell or not expressed where expressed in a control cell.

As used herein, the term "polypeptide" is defined as a compound of two or more subunit amino acids, amino acid analogs, or peptidomimetics. The subunits may be linked by peptide bonds. In another embodiment, the subunit may be linked by other bonds, e.g., ester, ether, etc. As used herein the term "amino acid" includes either natural and/or unnatural or synthetic amino acids, including glycine and both the D or L optical isomers, and amino acid analogs and peptidomimetics. A peptide of three or more amino acids is commonly referred to as an oligopeptide. Peptide chains of greater than three or more amino acids are referred to as a polypeptide or a protein.

As used herein, the term "marker" is defined as a polynucleotide or polypeptide molecule which is present or absent, or increased or decreased in

quantity or activity in subjects afflicted with multiple sclerosis, or in cells involved in multiple sclerosis. The relative change in quantity or activity of the marker is correlated with the incidence or risk of incidence of multiple sclerosis or progression from one stage of the disease to another.

Although all of the markers listed in Tables I-V can be used in diagnosis of MS, an additional object of the present invention was to identify those markers which can be utilized to diagnose specific clinical forms and/or stages of MS.

Accurate clinical tools for specific diagnosis of disease stages in MS are presently unavailable.

As a result of comprehensive studies conducted in efforts to evaluate specific gene expression in relation to clinical disease phases, the present invention provides, for the first time, specific markers sets which can be utilized in accurate diagnosis of specific forms and stages of MS

As is illustrated in Example II of the Examples section which follows, the present invention provides marker sets which can be accurately utilized to diagnose acute relapse, remission and probable stages of MS (Tables III-V).

Of particular importance is the marker set provided in Table V. As is described in the Examples section which follows, the present inventors also uncovered cellular markers which distinct between disease-related and non-disease related T-cell myelin reactivity. Although MS appears to be caused by autoimmune T-cells activated against myelin self-antigens, myelin-reactive T-cells have been demonstrated in healthy subjects as well. Thus, distinction between disease-related and non-disease related T-cell myelin reactivity is of great clinical and investigational importance.

Cellular markers which distinct between disease-related and non-disease related T-cell myelin reactivity include down-regulating apoptosis associated genes, up regulating anti-apoptotic genes and genes responsible for increased expansion capability of autoreactive T cells and enhanced ability to penetrate

the CNS. Thus, the markers of Table V include genes involved in perpetuating pathologic cellular proliferation and tissue destruction within the CNS characteristic of MS, along with increased resistance to regulation. This marker set accurately defines the requirements for an individual to develop MS, and thus has important predictive value, especially in diagnosing individuals having MS in the "probable" stage.

The identification of these markers significantly advances the field of MS diagnosis and treatment as well as provides tools which will enable elucidation of the mechanisms underlying MS formation and progression, ultimately leading to formulation of efficient, stage specific, treatment regimens.

The markers of the invention may be nucleic acid molecules (e.g., DNA, cDNA, or RNA) or the polypeptides encoded thereby. As such, detection of markers in a sample obtained from an individual can be effected using various detection methods well known to the ordinary skilled artisan.

Briefly, measurement of the relative amount of nucleic acid or polypeptide molecules can be effected by any method known in the art (see, e.g., Sambrook, J., Fritsh, E. F., and Maniatis, T. Molecular Cloning: A Laboratory Manual. 2nd, ed, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989; and Current Protocols in Molecular Biology, eds. Ausubel et al. John Wiley & Sons: 1992). Typical methodologies for RNA detection include RNA extraction from a cell or tissue sample, followed by hybridization of a labeled probe (e.g., a complementary nucleic acid molecule) specific for the target RNA to the extracted RNA, and detection of the probe (e.g., Northern blotting). Typical methodologies for polypeptide detection include activity assays in cases of known enzymes, protein extraction from a cell or tissue sample, followed by hybridization of a labeled probe (e.g., an antibody) specific for the target protein to the protein sample, and detection of the probe. The label group can

be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Detection of specific polypeptide and nucleic acid molecules may also be assessed by gel electrophoresis, column chromatography, direct sequencing, or quantitative PCR (in the case of nucleic acid molecules) among many other techniques well known to those skilled in the art.

Probes based on the nucleotide sequence of a marker gene or of a nucleic acid molecule encoding a marker polypeptide of the invention can be used to detect transcripts or genomic sequences corresponding to the marker gene(s) and/or marker polypeptide(s) of the invention. In preferred embodiments, the probe comprises a label group attached thereto, e.g., the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress (e.g., over- or under-express) a marker polypeptide of the invention, or which have greater or fewer copies of a marker gene of the invention. For example, a level of a marker polypeptide-encoding nucleic acid in a sample of cells from a subject may be detected, the amount of mRNA transcript of a gene encoding a marker polypeptide may be determined, or the presence of mutations or deletions of a marker gene of the invention may be assessed. The invention further encompasses nucleic acid molecules that differ from the nucleic acid sequences of the genes set forth in Tables I-V, due to degeneracy of the genetic code and which thus encode the same proteins as those encoded by the genes shown in Tables I-V.

An isolated marker protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind marker proteins using standard techniques for polyclonal and monoclonal antibody preparation. A full-length marker protein can be used or, alternatively, the invention provides antigenic peptide fragments of these proteins for use as immunogens. The antigenic peptide of a marker protein comprises at least 8 amino acid residues of an amino acid sequence encoded by a gene set forth in Tables I-V, and

encompasses an epitope of a marker protein such that an antibody raised against the peptide forms a specific immune complex with the marker protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the marker protein that are located on the surface of the protein, e.g., hydrophilic regions, as well as regions with high antigenicity.

An anti-marker protein antibody (e.g., monoclonal antibody) can be used to isolate a marker protein of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-marker protein antibody can facilitate the purification of natural marker proteins from cells and of recombinantly produced marker proteins expressed in host cells. Moreover, an anti-marker protein antibody can be used to detect marker protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the marker protein. Anti-marker protein antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase,

luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (J. Mol. Biol. 1990;215:403-10). BLAST nucleotide searches can be performed with the NBLAST program, score=100, wordlength=12 to obtain nucleotide sequences homologous to nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to marker protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) Nucleic Acids Res. 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See http://www.ncbi.nlm.nih.gov.

It will be appreciated that non-coding sequences, such as promoter or other regulatory sequences of marker genes may be used as probes in the context of the present invention. Thus, the expression of groups of functionally related genes, responsive to similar signals important to the pathogenesis or progression of multiple sclerosis, may be assessed.

It will be appreciated that in certain cases the genes themselves can serve as markers. For example, mutations in the nucleic acid sequence of a gene (e.g., non-sense, mis-sense deletion and the like) which result in lower expression levels of the gene or lower activity of the gene product may be correlated with MS. Similarly, a duplication of the gene, which can result in higher expression levels or mutations which result in higher activity can also be correlated with MS.

Detection of the presence or number of copies of all or a part of a marker gene of the invention may be performed using any method known in the art. Typically, it is convenient to assess the presence, quantity and quality of genomic DNA by Southern analysis, in which total DNA from a cell or tissue sample is extracted, is hybridized with a labeled probe (e.g., a complementary DNA molecule), and the probe is detected. The label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Other useful methods of DNA detection and/or quantification include direct sequencing, gel electrophoresis, column chromatography, and quantitative PCR, as is known by one skilled in the art.

In cases where detection involves discrete marker sets, the detection method of the present invention preferably employs marker probes which are conjugated to a solid support. For example, polynucleotide probes capable of specifically hybridizing with polynucleotide markers of the present invention (e.g., mRNA) may be coupled to an array (e.g., a GeneChip array for hybridization analysis), to a resin (e.g., a resin which can be packed into a column for column chromatography), or a matrix (e.g., a nitrocellulose matrix for northern blot analysis). The immobilization of molecules complementary to the marker(s), either covalently or noncovalently, permits a discrete analysis of the presence or activity of each marker in a sample. In an array, for example, polynucleotides complementary to each member of a marker set may individually be attached to different, known locations on the array (region-specific arrays). The array may be hybridized with, for example, polynucleotides extracted from a blood sample obtained from a subject. The hybridization of polynucleotides extracted from the sample with the array at any location on the array can be detected, and thus the presence or quantity of the marker in the sample can be ascertained. In a preferred embodiment, a "GeneChip" array is employed (e.g., an Affymetrix type array). Similarly, Western analyses may be performed on immobilized antibodies specific for

different polypeptide markers hybridized to a protein sample from a subject.

It will also be apparent to one skilled in the art that the probes of the array need not bind with the entire marker molecule. A probe designed to bind a portion of the marker of sufficient length for detection purposes (e.g., for hybridization), for example, a portion of the marker which is 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 100 or more nucleotides or amino acids in length may be sufficient for detection purposes.

Polynucleotide probes can be synthesized using any known synthesis method. Preferably, synthesis is effected using on-chip lithography methodology in a manner similar to that utilized for the synthesis of Affymetrix chips (www.affymetrix.com). Additional methods of array production and methodology are described in detail in the U.S. Patent Applications cited in the Background section hereinabove.

Antibody probes useful for detecting polypeptide markers can be generated using various well known techniques. For example, monoclonal antibodies which can be used per se or as a basis for antibody fragments (scFv, Fab etc) can be synthesized using isolated Hybridomas. In such an approach, a protein corresponding to a marker of the invention is isolated (e.g., by purification from a cell in which it is expressed or by transcription and translation of a nucleic acid encoding the protein in vivo or in vitro using known methods. A vertebrate, preferably a mammal such as a mouse, rat, rabbit, or sheep, is immunized using the isolated protein or protein fragment. The vertebrate may optionally (and preferably) be immunized at least one additional time with the isolated protein or protein fragment, so that the vertebrate exhibits a robust immune response to the protein or protein fragment. Splenocytes are isolated from the immunized vertebrate and fused with an immortalized cell line to form hybridomas, using any of a variety of methods well known in the art. Hybridomas formed in this manner are then screened

using standard methods to identify one or more hybridomas which produce an antibody which specifically binds with the protein or protein fragment.

The invention also includes an array comprising a marker(s) of the present invention. The array can be used to assay expression of one or more genes in the array.

In one embodiment, the array can be used to assay gene expression in a tissue of multiple sclerosis patients at different stages of the disease to ascertain stage specificity of genes in the array. In this manner, more than about 30,000 genes can be simultaneously assayed for expression. This allows a profile to be developed showing a battery of genes specifically expressed in one or more stages of the disease.

In addition to such qualitative determination, the invention allows the quantitation of gene expression. Thus, not only stage specificity, but also the level of expression of a battery of stage specific genes is ascertainable. Thus, genes can be grouped on the basis of their expression per se, and level of expression in that stage of the disease.

The detection arrays described herein are preferably packaged in kits identified for use in detecting MS in general or for detecting specific stages of MS. The kit can further include reagents suitable for the detection of polynucleotide hybridization or antibody binding and instructions for effecting diagnosis using the kit components and suitable detection hardware (e.g., detection microscope) and software (e.g., detection and analysis software). For further description of such hardware and software and detection reagents please see www.affymetrix.com.

Thus, the present invention provides methods useful for diagnosing MS including specific stages or states of the disease and also a risk of developing the disease.

These methods involve isolating a sample from a subject (e.g., a sample containing T-cells), detecting the presence, quantity, and/or activity of one or

more markers of the invention in the sample relative to a normal sample. Observing a significant increase or decrease in one or more markers in the test sample indicates the presence or risk of presence of MS.

Using specific marker sets, the present invention also provides methods of assessing the severity or stage of MS in a subject.

As detailed hereinabove, a major concern in treatment of multiple sclerosis is accurate early diagnosis following the first acute attack. At present, clinical studies indicate that only 40-50% of individuals suffering a first acute attack will progress to clinically definite MS. Thus, treatment protocols most commonly suspend treatment of these patients defined as probable MS, until the appearance of a second attack, which may entail years of waiting and uncertainty. It will be appreciated that early and accurate detection of the portion of probable MS patients likely to progress to further stages of the disease can save undue suffering and expense, and, more importantly, provide early treatment and a better prognosis for the portion of probable MS patients likely to progress to more severe stages. The present invention provides, for the first time, marker genes for probable MS, as well as for relapsing vs. remitting MS.

The present invention also provides methodology which can be used to assess the efficacy of an MS treatment regimen and/or the effect of environmental factors or diet on the progression of MS.

These methods involve isolating a sample from a subject (e.g., a sample containing T-cells) suffering from MS who is undergoing treatment which includes drug therapy, exposure to a predetermined environmental condition and/or a specific diet, detecting the presence, quantity, and/or activity of one or more markers of the invention in test samples obtained from the subject prior to and following treatment or in a test sample obtained from the subject relative to a sample obtained from an individual suffering from MS who is not undergoing any treatment and/or relative to a sample obtained from an individual not

suffering from MS and undergoing treatment. The levels of markers in the samples are compared, and significant increases or decreases in one or more markers in the test sample following treatment relative to the other samples are observed, and correlated with the severity or stage of MS. By assessing whether MS has been lessened or alleviated, the ability of the treatment or therapy to treat MS is also determined.

It will be appreciated that the present invention also provides methods of treating (e.g., inhibiting) the formation or progression of MS. These methods involve isolating a sample from a subject (e.g., a sample containing PMBCs such as T-cells), detecting the presence, quantity, and/or activity of one or more markers of the invention in the sample relative to a normal sample and observing significant increases or decreases in one or more markers in the test sample. For markers that are significantly decreased in expression or activity, the subject may be administered that expressed marker protein, or may be treated by the introduction of mRNA or DNA corresponding to the decreased marker (e.g., by gene therapy), to thereby increase the levels of the marker protein in the subject. For markers that are significantly increased in expression or activity, the subject may be administered mRNA or DNA antisense to the increased marker (e.g., by gene therapy), or may be administered antibodies specific for the marker protein, to thereby decrease the levels of the marker protein in the subject. In this manner, the subject may be treated for MS or MS related condition.

In another embodiment, the methods further involve obtaining a control biological sample (e.g., nondiseased tissue) from a control subject, contacting the control sample with a compound or agent capable of detecting marker protein, mRNA, or genomic DNA, such that the presence of marker protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of marker protein, mRNA or genomic DNA in the control sample

with the presence of marker protein, mRNA or genomic DNA in the test sample.

The invention also provides methods for identifying modulators, i.e., candidate or test compounds or agents (e.g., peptides, peptidomimetics, peptoids, small molecules or other drugs) which (a) bind to the marker, or (b) have a modulatory (e.g., stimulatory or inhibitory) effect on the activity of the marker or, more specifically, (c) have a modulatory effect on the interactions of the marker with one or more of its natural substrates (e.g., peptide, protein, hormone, co-factor, or nucleic acid), or (d) have a modulatory effect on the expression of the marker. Such assays typically comprise a reaction between the marker and one or more assay components. The other components may be either the test compound itself, or a combination of test compound and a natural binding partner of the marker. The test compounds of the present invention may be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. Test compounds may also be obtained by any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive; (see, e.g., Zuckermann et al., 1994, J. Med. Chem. 37:2678-85); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the `one-bead one-compound` library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, Anticancer Drug Des. 12:145).

Additional objects, advantages, and novel features of the present invention will become apparent to one ordinarily skilled in the art upon

examination of the following examples, which are not intended to be limiting. Additionally, each of the various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below finds experimental support in the following examples.

EXAMPLES

Reference is now made to the following examples, which together with the above descriptions, illustrate the invention in a non limiting fashion.

Generally, the nomenclature used herein and the laboratory procedures utilized in the present invention include molecular, biochemical, microbiological and recombinant DNA techniques. Such techniques are thoroughly explained in the literature. See, for example, "Molecular Cloning: A laboratory Manual" Sambrook et al., (1989); "Current Protocols in Molecular Biology" Volumes I-III Ausubel, R. M., ed. (1994); Ausubel et al., "Current Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York; Birren et al. (eds) "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998); methodologies as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057; "Cell Biology: A Laboratory Handbook", Volumes I-III Cellis, J. E., ed. (1994); "Culture of Animal Cells - A Manual of Basic Technique" by Freshney, Wiley-Liss, N. Y. (1994), Third Edition; "Current Protocols in Immunology" Volumes I-III Coligan J. E., ed. (1994); Stites et al. (eds), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (eds), "Selected Methods in Cellular Immunology", W. H. Freeman and Co., New York (1980); available immunoassays are extensively described in the patent and scientific literature, see, for example, U.S. Pat. Nos. 3,791,932; 3,839,153; 3,850,752; 3,850,578;

3,853,987; 3,867,517; 3,879,262; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; 4,098,876; 4,879,219; 5,011,771 and 5,281,521; "Oligonucleotide Synthesis" Gait, M. J., ed. (1984); "Nucleic Acid Hybridization" Hames, B. D., and Higgins S. J., eds. (1985); "Transcription and Translation" Hames, B. D., and Higgins S. J., eds. (1984); "Animal Cell Culture" Freshney, R. I., ed. (1986); "Immobilized Cells and Enzymes" IRL Press, (1986); "A Practical Guide to Molecular Cloning" Perbal, B., (1984) and "Methods in Enzymology" Vol. 1-317, Academic Press; "PCR Protocols: A Guide To Methods And Applications", Academic Press, San Diego, CA (1990); Marshak et al., "Strategies for Protein Purification and Characterization - A Laboratory Course Manual" CSHL Press (1996); all of which are incorporated by reference as if fully set forth herein. Other general references are provided throughout this document. The procedures therein are believed to be well known in the art and are provided for the convenience of the reader. All the information contained therein is incorporated herein by reference.

MATERIALS AND METHODS

Subjects - Blood was obtained from patients or controls after written informed consent. *For comparison of healthy controls and MS patients, and between MS patients in acute relapse or remission*: Gene expression profiles of 26 patients (20 females, mean age 41.0±2.5 years) with definite diagnosis of MS according to Poser criteria (8), a relapsing-remitting disease course, and brain magnetic resonance imaging ascertaining the diagnosis (9) were compared with eighteen (18) age-matched healthy subjects (16 females). *For comparison of transcriptional profiles in MOG-reactive T-cells*: Four MS female patients (mean age 38±4.2 years, mean disease duration 9.3±3.3 years) having a definite MS according to Poser criteria (10), a relapsing-remitting disease course, neurological disability evaluated by the expanded disability status scale (EDSS, 11) between 2 to 5.0, and brain MRI supporting the

diagnosis of MS, and three age- and sex-matched healthy controls were included in the study. None of the patients received immunomodulatory drugs or steroid treatment for at least three months prior to when blood was drawn. The studies were approved by the institutional review board and the Israel Ministry of Health.

mRNA preparation - Total RNA was isolated from Ficoll™ isolated Peripheral Blood Mononuclear Cells (PBMC) or from MOG-stimulated T cell lines ($2x10^7$ cells) by ice-cold TRIZOL Reagent (Gibco, BRL). Poly-A mRNA was isolated using a mini-kit (Oligotex, Qiagen) and used as a template for double-stranded cDNA synthesis using oligo (dT)-24 primers containing a T7 RNA polymerase promoter site added to the 3'- end (Genset). After phenol/chloroform extraction cDNA was used as a template for *in vitro* transcription (Ambion T7 Megascript system) with biotin labeled nucleotides (Enzo Diagnostics). Labeled cRNA was fragmented, quantified by spectrophotometer, and hybridized to the microarrays.

Microarray gene analysis - Each Genechip (U95Av2) which carries probes for 12,625 (or U133A with 22,000 for patients with probable MS diagnosis) transcripts was hybridized with 10μg/200μl hybridization mix, stained and scanned (Hewlett Packard, GeneArray-TM scanner G2500A) according to manufacturer protocol (Affymetrix Inc, Santa Clara, CA). Scaling procedure was performed to an average intensity of 600 per gene. A value of 20 was assigned to all measurements lower then 20. *For comparison of healthy controls and MS patients, and between MS patients in acute relapse or remission*: All data was normalized by dChip software and fold ratios were calculated for each gene of the samples against geometric means of the matched controls. *For comparison of transcriptional profiles in MOG-reactive T-cells*: Genes that did not have at least one average difference intensity value $\geq$100 or were present at least once by Affymetrix criteria, were not included in the analysis.

Data analysis - The analysis was performed according to the analytical approach as previously described (24-26). Genechip 4 software (Affymetrix Inc, Santa Clara, CA) was used for analysis of the scanned arrays. Fold ratios were calculated for each gene of the samples against the geometric mean of matched controls. *For comparison of transcriptional profiles in MOG-reactive T-cells*: To determine the most informative genes threshold number of misclassifications (TNoM) score was applied. This score counts the number of classification errors that occur between compared groups for each gene of the dataset. The best threshold (TNoM=0) implies that no errors have been counted and the distinction between the two groups in relation to the expression level of a specific gene is maximal. To select a group of strongly differential expression, t-test p-value (comparing expression levels of genes from MS patients vs. healthy controls) were also computed. Genes with TNoM = 0, fold-change >1.5 (either up or down regulated) and corresponded t-test P value < 0.05, were designated as most informative. *For comparison of healthy controls and MS patients, and between MS patients in acute relapse or remission*: The data was analyzed by the classic parametric t-test, and the following non-parametric tests: (i) Threshold number of misclassifications (TNoM) method and (ii) INFO score that measures the misclassifications made by a simple threshold in terms of the information lost. Analysis was performed between MS patients and the control group for each gene of the dataset as well as between subgroups of patients. Only informative MS related genes ($p<0.05$ in all three statistical tests) were included. To retrieve the most informative genes, the False Discovery Rate (FDR) method (14) that ranks and tests all "P" values against different thresholds was used. The degree of significance by the Bonferroni threshold method, which evaluates the allowed error probability divided by the number of genes measured, and ensures that each and every validated scoring event is indeed a significant event, was also calculated.

Validation Strategy - To further assess the predictive power of the data sets, computerized analysis by the Leave-One-Out-Cross-Validation (LOOCV) statistical method was performed. The method simulates removal of a single sample every trial and trains on the rest. The procedure is repeated until each sample is left out once and the number of correct and incorrect predictions is counted.

EXAMPLE I

Accurate Gene Expression Profiles of MS

In order to provide an accurate, reliable profile of gene markers for diagnosis and evaluation of MS, DNA chip analysis was used to compare multiple gene expression patterns of PBMCs from patients with different clinical forms of MS. After informed consent blood was obtained from 26 patients (20 females, mean age 41.0±2.5 years) with definite diagnosis of MS according to Poser criteria, a relapsing-remitting disease course, and brain magnetic resonance imaging ascertaining the diagnosis. Eighteen age-matched healthy subjects (16 females) served as controls. PBMC gene expression of 12,625 human genes was analyzed as described hereinabove, using Ficoll™ for preparation of PBMCs and total RNA purification and sample preparation according to the instructions of Affymetrix, Inc (Affymetrix, Santa Clara CA, USA). In order to determine the most informative genes, unique computerized scoring methods, as yet not applied to analysis of data regarding MS, were employed. In brief, a gene is designated as informative based on the degree to which its tissue expression level is predictive of an independent classification of the tissue sample as "diseased" or "not diseased", as previously described by Ben-Dor et al (J Comput Biol 2000;7:559-63) and applied to the analysis of breast cancer and melanoma using cDNA arrays (for review see Freidman N et al Ernst Schering Res Found Wkshp 2002;38:109-31). The scores used in this study were:

TNoM (Total Number of Misclassifications) - the number of classification errors committed when using the best simple threshold to distinguish between two classes (diseased or not diseased) based on the expression levels of a specific gene.

INFO - an estimate of the uncertainty remaining about accuracy of a sample classification (diseased or not diseased) after the incorporation of

predictions based on expression of an individual gene is given (a lower "INFO" score indicates a higher predictive value for a given gene).

Gaussian (t-test) - The overlap between distributions of expression levels for genes in two classes. The score is based on normality assumptions.

One of the advantages of the analytic methods used here is their amenability to rigorous statistical benchmarking. Using this unique analysis, the number of informative genes per score expected in a random classification can be calculated, and then this estimated number of high scoring (or informative) genes can be compared to the actual number of informative genes (per score) measured in a dataset.

Comparison of the gene expression profiles shows that gene expression of PBMC in MS patients is significantly different from that in healthy subjects. Under the null-hypotheses that the separation of the samples is random despite genetic heterogeneity between tested groups, observed significant overabundance of informative genes was observed (Fig. 1A). The difference between expected and observed number of genes with significant p value in all 3 statistical tests (t-test, TNoM, INFO) performed, indicates that the diversity in gene expression observed in PBMC is biologically significant.

The predictive power of the data sets results was assessed by performing computerized error estimates based on *leave-one-out cross validation* (LOOCV) trials. The results disclosed only 3 classification errors. This low rate of error estimates suggest that the gene expression signature in MS is reliable for the diagnosis of the disease using peripheral blood and confirms that the patterns we observed accurately represent significant biologic phenomena associated with MS. The false discovery rate (FDR) method distinguished 1249 most informative genes that pass 95% FDR on all three statistical tests (t-test, TNoM, INFO) at $p < 0.05$ (Fig. 1B and Table I).

Confirmation of gene microarray expression findings was performed by RT-PCR for the following five randomly selected genes: EGFL5, P44, GS3686,

MX1 and CCR2. Significant correlations (coefficients ranged from 0.76 to 0.98) were found between the relative number of expression genes analysis and the RT-PCR profile. The data from microarray hybridizations was further tested against the strict Bonferroni threshold method from all three statistical tests, as described hereinabove, resulting in 300 top scoring genes that distinguish between MS and healthy subjects. (Table II).

The 1249 most informative genes (681 up-regulated, 569 down-regulated, Table I) consist of inflammatory, apoptosis and cell signaling pathways components, cytokines, antigen presentation molecules and chemokines as well as number of expressed sequence tags (ESTs).

Over-expressed genes in MS - The most abundant over-expressed transcripts unique to MS include: (i) **SLAM** (signaling lymphocyte activation molecule) a member of the immunoglobulin gene superfamily that is involved in T-cell stimulation. SLAM potentiates T-cell expansion and was described as CD28 independent co-stimulatory molecule, selectively increasing interferon gamma production and dysregulating type 1 and type 2 cytokine production in MS upon T-cell receptor activation. The surprising observation of SLAM upregulation suggests an enhanced proliferation of autoreactive T cells in MS patients; (ii) **LEF1** (lymphoid enhancer-binding factor 1) one of the transcriptional factors expressed in pre-B and T cells, and known to be associated with T cell receptor (TCR) stimulation and apoptosis survival of pro-B cells (19); (iii) **LRP5** (low density lipoprotein receptor-related protein 5) a of cell receptor protein required for LEF1 activation; (iv) **LILRB** (leukocyte immunoglobulin-like receptor), a protein that binds MHC class I molecules and delivers a negative signal inhibiting killing by natural killer and regulatory T cells; (v) **LY75** (lymphocyte antigen 75) an endocytotic receptor used by dendritic cells to direct captured antigens from the extracellular space to a specialized antigen-processing compartment; and (vi) **CDW52**, a 21-28 kDa glycopeptide antigen expressed on lymphocytes and macrophages known to be

a target for complement-mediated insult, inducing pro-inflammatory cytokine (e.g. TNF alpha and interferon gamma) production. Other up-regulated genes are members of the anti-apoptotic pathways, and include **PIP5K1-gamma** (Phosphatidylinositol-4-phosphate 5-kinase, type 1, gamma) and **MAP4** (Microtubule-associated protein 4). Over-expression of transcripts belonging to the papain cysteine proteinase family **CTSK** (Cathepsin K) and **CTSB** (Cathepsin B) was also observed.

Down-regulated genes in MS - Abundant down-regulated transcripts unique to MS that were identified include **IL1B** (Interleukin 1 beta), an important inflammatory cytokine; **TRAF6,** which is essential for IL1 signaling; and **SCYA20**, known to be mediated by IL1B. Decreased mRNA expression of **IL1B** was strengthened by the down regulation of **IL1R** (type1 receptor), **IL1RAP** (receptor accessory protein) and **IL1RN** (receptor antagonist).

Other important down-regulated genes include **TGFB1** (Transforming growth Factor beta 1) and **SKI** (v-ski sarcoma viral oncogene homologue) a component of TGFB signaling pathway, both known to inhibit cell proliferation. Thus, their under expression may contribute to autoreactive T cell expansion. Members of epidermal growth factor family such as **VEGF** (Vascular endothelial growth factor), **IGFBP4** (Insulin-like growth factor binding protein 4) and **EREG** (epiregulin) were also down regulated. Additionally, mRNA expression of members of the steroid-thyroid receptors family including nuclear receptor subfamily 4, group A members 1, 2 and 3 (**NR4A1, NR4A2, NR4A3**) were significantly reduced. Down regulation of these genes may inhibit apoptosis through Fas ligand and tumor necrosis factor alpha or through early response of T-cell receptor induced apoptosis of thymocytes, thus mimicking positive selection.

Taken together, the identification of profiles of up- (overexpressed) and down regulated genes specific to MS indicates the suitability of the methods of the present invention for identifying validated and significant molecular

signatures of PBMC gene expression in MS. While reducing the present invention to practice, it was observed that the specific disease related genes include transcripts involved in T cell activation and expansion and anti-apoptotic mediators, indicating failure of apoptosis-related elimination of autoreactive T cells.

EXAMPLE II

Stage Specific Gene Expression Profiles of MS

Accurate clinical tools for specific diagnosis of disease stages in MS are presently unavailable. In order to provide a useful profile of the clinically defined stages of MS, specific gene expression was evaluated in relation to clinical disease phases. Significant overabundance was found between the number of observed and expected genes expressed in MS patients during an acute relapse and in remission (Fig. 2A). Using the methods described hereinabove, the 743 most informative genes (302 up-regulated and 441 down-regulated) with p-value < 0.05 in all three scores (t-test, TNoM, INFO) that differentiated relapse from remission (Fig 2B, Table III) were identified.

Over-expressed genes in acute relapse of MS, compared to patients in remission - The most informative over-expressed genes included **CTSL** (Lysosomal cystein protease L, cathepsin L) known to play a role in MHC class II antigen presentation, responsible for quantitative and qualitative difference in peptide repertoires displayed by MHC class II molecules, and having a regulatory role in epitope generation for antigens subsets. Moreover, in vitro, proteolytic **CTSL** processed myelin basic protein into more then 60 different 20-40-mers species, and myelin-associated glycoprotein was described as a substrate for **CTSL** like proteases. These data, taken together with our observation that **CTSL** mRNA was over expressed in the active stage of MS, offer a biochemical basis for the immunodominant epitope spreading implicated in the pathogenesis of MS. Also up-regulated is **SCYA2** (Monocyte

specific chemoattractant protein, MCP1), essential for monocyte and NK cells recruitment to site of inflammatory injury. Augmented **SCYA2** expression level in the CNS has been identified at the onset of EAE. Other abundant up-regulated transcripts identified by the method of the present invention include **CD79A**, **DDIT3** (DNA-damage inducible transcript 3); **E2-EPF** (Ubiquitin carrier protein) and **COX6**.

Downregulated genes in acute relapse of MS, compared to patients in remission - From the downregulated gene transcripts in acute relapse vs. remission it is important to note several programmed cell death-related genes like **CCNG1** (Cyclin G1) identified as p53 dependent apoptosis; **PDCD2** (Programmed cell death 2) expressed in immature thymocytes; and **CTLA1** (Cytotoxic T lymphocyte associated serine esterase 1), crucial for the rapid induction of apoptosis by cytotoxic cells. Also prominently downregulated during acute relapse was **JAK1** (Janus kinase 1), a protein tyrosine kinase reported to be obligatory for several cytokines receptors, important for regulation of acute cellular response.

The results of the functional annotation of the transcriptional motifs that distinguish between acute MS relapse and remission suggest that many of the genes are involved in cellular recruitment and epitope spreading, as well as important to immunologic mechanisms related to escape from regulatory surveillance and augmentation of cell survival potential. Thus, it can be suggested that during the acute inflammatory process of the disease there is a failure of the immune regulatory cells to inhibit autoreactivity and the self-expansion of the non-restrained autoreactive T cells further lead to a vicious cycle of on going inflammatory activity.

It is evident from the gene-clustering map (Fig 2B) that during an acute relapse no significant differences are found between relapse treated vs. relapse untreated patients. Such a result is of great clinical significance, since this may indicate that during an acute MS exacerbation the major gene expression

transcripts are related to relapse associated genes and the effect of therapy is negligible. However, during remission treatment effect was more pronounced and this effect on gene suppression in treated patients was evident.

Of even greater significance is the demonstration, for the first time, of a specific gene expression profile of the "probable" stage of MS. As described hereinabove, "probable" MS precedes definitive clinical diagnosis, and is characterized by diverse neurological symptoms including unilateral loss of vision, true vertigo, ataxia, paresthesia, incontinence, diplopia, dysarthria or paralysis. Probable MS patients may suffer undiagnosed for years. In order to provide a method for accurate diagnosis of probable MS, in advance of onset of clinical symptoms, gene expression in PBMC samples of 13 probable MS patients were compared with that of samples from 5 age-matched healthy controls. RNA preparation, hybridization to MicroArray and analysis of results was performed as described for Examples 1 and 2, and in the Material and Methods section hereinabove.

As is shown in Table V, a specific "probable" MS profile of gene expression distinguishes PBMCs of diseased and healthy individuals.

Thus, there is demonstrated, for the first time, gene expression profiles providing criteria for distinguishing between stages of MS in humans, for example, between relapsing and remitting MS, probable MS and healthy individuals. Further, the groups of up- and down-regulated genes identified herein may be used for investigation of mechanisms of disease and disease progression in MS.

EXAMPLE III

Gene Expression Profiles in Treatment of MS

The effect of immunomodulatory treatment on gene expression in MS patients was investigated by comparison analysis of gene transcripts between treated and untreated patients. Suprisingly, despite the variety of

immunomodulatory treatments and differences between patients in relation to treatment duration, the microarray methods described herein, treatment-related gene transcripts that differentiated between treated and untreated patients were detected. Treatment-specific gene expression is mainly associated with phosphorylation and signal transduction. Thus, gene microarray technology can be a powerful tool in evaluating and monitoring clinical correlations of effects of treatment, and determining prognosis.

Thus, data presented herein demonstrate for the first time distinct and significant fingerprint cluster in MS patients that differentiates them from healthy subjects. Moreover, the stringent and specific fingerprint is predictive for the diagnosis of MS and is suitable for guiding the selection of patients for early treatment. Additionally, separate gene expression patterns were identified between acute MS relapse and remission, and treatment effects could also be identified. The methods described herein may also be used to offer superior insight into the biological mechanisms involved in the disease as well as improving functional gene characterization and transcription sites detection, important for identification of new targets for treatment and drug identification, such as T cell activation and expansion and anti-apoptotic genes like **SLAM**, **PIP5K1-g** and the **NR4A1-3** steroid-thyroid receptors subfamily.

EXAMPLE IV

Gene Expression Profiles of MOG-Reactive T-cells from MS Patients

Although MS appears to be caused by autoimmune T cells activated against myelin self-antigens, myelin-reactive T-cells have been demonstrated in healthy subjects as well. Thus, distinction between disease-related and non-disease related T-cell myelin reactivity is of great clinical and investigational importance. In order to determine a profile of MS-related T-cell genes, gene expression in MOG-reactive T-cells from 4 MS patients having relapsing-

remitting disease course, positive Poser criteria, and neurological disability, and 3 healthy age-matched controls was compared.

Using the microarray methods described herein, gene expression patterns obtained in MOG reactive T cell lines from MS patients detected 150 transcripts with TNoM=0, p=0.057 compared to healthy subjects (Figure 4). These high scoring gene transcripts were defined as significant MOG reactive MS-related genes. Hierarchical clustering of gene expression patterns from MS patients and healthy controls is presented in Figure 2, panel A. From the 150 genes with absolutely different expression levels, 43 most informative genes were further identified and clustered. These include 18 up-regulated and 25 down-regulated genes (Figure 2, panel B).

Investigation of the known biological function of these genes (Table V) shows a great diversity of activity (A Pie-chart diagram showing the functional groups of genes included in this evaluation is presented in Figure 3). Included are genes coding for proteins involved in the regulation and execution of apoptosis, growth factors, mediators of signal transduction pathways, molecules that participate in inflammation and also genes encoding heat shock proteins, transcription factors and components of different biochemical pathways.

Upregulated Genes in MS-Derived T-cells - Up-regulated in MS patient-derived T-cell lines are several anti-apoptotic genes such as **BCL2**, **lifeguard**, and the MAP-activated kinase **MAP3K12**. The **BCL2** gene product is an important member of the anti-apoptotic proteins. Lifeguard (**LFG**), is a molecule that inhibits cell death mediated by the Fas (CD95) receptor through a unique mechanism that down regulates apoptotic signals from Fas and is associated with human autoimmune lymphoproliferative syndrome (ALPS) and in lymphoproliferative lupus-like syndrome in mice.

The MAP3K12 gene is associated with programmed cell death and encodes a polypeptide that catalyzes the phosphorylation of BAD, a member of the BCL2 anti-apoptosis protein family. Increased expression of **IGFBP3** and

VEGF was also demonstrated in MS-derived T cells. **IGFBP-3** has been implicated in the expansion of disease related T-cell, associated with acute brain lesions of MS patients. Thus, in addition to increased survival potential, our findings suggest that autoreactive T cells in MS also have an expansion advantage compared with T cells from healthy individuals.

Furthermore, migration of autoimmune T cells into the brain would be expected to be assisted by over-expression of transcripts encoding for vascular endothelial growth factor (**VEGF**) in lines from MS patients. **VEGF** enhances vascular permeability and may facilitate migration of lymphocytes into the CNS and induction of inflammatory reactions in the brain.

Downregulated Genes in MS-Derived T-cells - The profile of gene expression in MS-derived T-cells (Figure 4, and Table V) indicates a suppression of apoptosis-related functions in the diseased state. One aspect of failure to induce apoptosis in the MS-derived T cell lines is the significant down-regulation of the gene encoding for the pro-apoptotic molecule **TNF**. A reduction in **TNF** could also contribute to a reduction in the ratio of pro- and anti-apoptotic transcript expression in the anti-MOG T cell lines from MS patients compared to healthy controls. Indeed, inadequate apoptosis present in MS autoreactive T cell lines could lead to insufficient deletion of autoimmune activated T cell clones and increase susceptibility to autoimmunity.

In addition, effectors of MHC class I presentation were revealed to be down-regulated in MS patients' cells. Such down-regulated expression includes the transcript for the **proteasome PA28 complex**, known to be a principal provider of MHC class I-presented peptides in antigen presenting cells, and **HSP70 1A and 1B** variants. **TNF** is also known to stimulate MHC class I presentation in addition to induction of apoptosis. The findings presented herein indicate that a weaker antigenic MHC class I presenting capability might distinguish MS-patient derived T cell lines from their healthy counterparts, and providing powerful diagnostic tools. It is conceivable that a lower expression of

MHC class-I on CD4 autoimmune T cells might enable them to escape regulation by CD8 cells that recognize autoimmune idiotypes.

Taken together the combined effects of down-regulation of apoptosis associated genes, up regulation of anti-apoptotic genes, increased expansion capability by autoreactive T cells and enhanced ability to penetrate the CNS may lead to perpetuated pathologic cellular proliferation and tissue destruction within the CNS characteristic of MS, along with increased resistance to regulation. The specific gene expression profiles described herein can define some of the requirements for an individual to develop MS, and thus have important predictive value, especially in determining MS in the "probable" stage. It is noteworthy that despite activation in vitro with the same MOG epitope, anti-MOG T cells from healthy subjects did not attain the gene expression profile that characterized the MS patient-derived cells. The findings support the concept that not all autoimmune T cells are equal; autoimmune T cells from MS patients follow a unique pattern of T cell activation that appears to be more resilient to apoptosis and can support long term survival. Although T cell lines derived from MS patients and healthy donors responded to the same autoantigen, were both activated T cell populations that proliferated extensively in the presence of IL-2, the gene expression imprints that are unique to each group were preserved. These findings indicate the existence of different T-cell activation mechanisms. The nature of the stimuli that generate aberrant autoimmune T-cell gene expression has yet to be identified in order to determine whether their formation is merely the result of the chronic immune stimulation driven by other factors in MS, or whether such T cells function as primary drivers of the MS process. Characterization of such driver T cells, dictating the state of immunity/autoimmunity can also greatly contribute to understanding autoimmunity and possibly also for designing effective treatments for MS.

TABLES I-V

Table I: Gene Expression Profile from PBMCs of MS vs. Healthy

SEQ ID NO:	Identifier	TNOM PValue	Info PValue	t-Test PValue	Log Fold Change	Symbol
1	U78107	8.55E-11	1.94E-11	4.04E-12	-0.43769	NAPG
2	M15330	8.55E-11	8.55E-11	2.49E-12	-2.13825	IL1B
3	X15218	8.55E-11	8.55E-11	1.40E-10	-1.41501	SKI
4	AF024710	8.55E-11	8.55E-11	1.13E-12	-1.95537	VEGF
5	U09937	1.84E-09	4.16E-10	2.04E-09	-1.21578	HSUROKR7
6	AB018343	1.84E-09	4.16E-10	9.05E-12	0.383078	KIAA0800
7	X74039	1.84E-09	4.16E-10	1.51E-10	-0.67381	PLAUR
8	M64571	1.84E-09	1.84E-09	2.41E-11	0.416659	MAP4
9	U64197	1.84E-09	1.84E-09	2.95E-10	-0.62373	SCYA20
10	X68452	2.57E-08	2.93E-09	9.12E-11	-0.26618	CCND2
11	AB011161	2.57E-08	2.93E-09	9.64E-11	0.63432	PIP5K1C
12	L47738	2.57E-08	2.93E-09	7.54E-09	0.31646	PIR121
13	U78798	2.57E-08	2.93E-09	1.11E-06	-0.3172	TRAF6
14	M63904	2.57E-08	7.16E-09	5.38E-09	-0.59612	GNA15
15	U72066	2.57E-08	7.16E-09	4.33E-08	-0.34482	RBBP8
16	AI184802	2.64E-07	1.61E-08	2.67E-09	-0.21576	HPRP4P
17	AF077820	2.64E-07	1.61E-08	2.91E-08	0.656852	LRP5
18	L13740	2.64E-07	1.61E-08	5.83E-08	-1.45891	NR4A1
19	AL008583	2.64E-07	1.61E-08	1.12E-08	0.250082	
20	Z24724	2.64E-07	1.61E-08	5.96E-09	-1.10426	
21	D30783	2.57E-08	2.19E-08	8.95E-10	-1.65011	EREG
22	U47927	2.57E-08	2.19E-08	5.53E-09	0.545592	USP5
23	AI560890	2.57E-08	2.19E-08	1.80E-07	0.179028	
24	Y00630	2.57E-08	3.69E-08	6.65E-09	-2.38485	SERPINB2
25	N90866	2.64E-07	8.23E-08	2.76E-08	0.304525	CDW52
26	AF022375	2.64E-07	8.23E-08	1.87E-11	-1.35847	VEGF
27	M24895	2.11E-06	1.08E-07	1.72E-08	0.476779	AMY2B
28	AF054176	2.11E-06	1.08E-07	6.47E-09	-0.58138	C1orf7
29	L20941	2.64E-07	1.08E-07	1.78E-06	-0.58618	FTH1
30	L05424	2.11E-06	1.08E-07	2.27E-09	-0.58081	HUMSCG19
31	AB002347	2.11E-06	1.08E-07	7.19E-10	0.371731	KIAA0349
32	AB023153	2.11E-06	1.08E-07	1.82E-08	0.895842	KIAA0936
33	AF069517	2.11E-06	1.08E-07	4.91E-07	0.399638	RBM6
34	X69392	2.64E-07	1.08E-07	1.10E-08	0.297444	RPL26
35	U51920	2.11E-06	1.08E-07	7.01E-08	-0.28142	SRP54
36	L22075	2.64E-07	1.71E-07	1.10E-08	-0.55736	GNA13
37	X04500	2.64E-07	1.71E-07	3.43E-10	-2.12121	IL1B
38	AB028951	2.64E-07	1.71E-07	8.78E-09	0.543028	KIAA1028
39	AF004230	2.64E-07	1.71E-07	3.06E-07	0.349166	LILRB1
40	AF070582	2.64E-07	1.71E-07	3.23E-08	-0.19773	MGC13033
41	X66363	2.64E-07	1.71E-07	6.53E-07	-0.24505	PCTK1

42	L33881	2.64E-07	1.71E-07	5.06E-08	-0.59585	PRKCI
43	U33017	2.64E-07	1.71E-07	5.20E-07	0.373581	SLAM
44	AJ007042	2.64E-07	1.71E-07	2.10E-07	0.170935	WHSC1
45	Z93930	2.64E-07	1.71E-07	2.42E-05	-0.39839	XBP1
46	AF079167	2.64E-07	1.71E-07	7.37E-10	-1.93249	
47	AF098641	2.64E-07	1.71E-07	1.56E-07	-0.41172	
48	HG3227-HT3404	2.64E-07	1.71E-07	1.68E-08	-0.25361	
49	U78302	2.64E-07	1.71E-07	2.41E-08	0.329878	
50	U91543	2.64E-07	2.49E-07	2.01E-07	0.478678	CHD3
51	M22919	2.64E-07	2.49E-07	9.52E-08	-0.81053	MYL6
52	AB029015	2.64E-07	2.49E-07	5.37E-09	0.695063	PLCE2
53	Z11697	1.37E-05	4.08E-07	3.55E-06	-1.21033	CD83
54	AL096780	1.37E-05	4.08E-07	2.13E-06	0.34487	CHKL
55	U51205	1.37E-05	4.08E-07	2.65E-07	-0.76279	COP9
56	Y08683	1.37E-05	4.08E-07	4.71E-06	0.492738	CPT1B
57	S52028	2.11E-06	4.08E-07	9.62E-08	-0.81662	CTH
58	X63368	2.11E-06	4.08E-07	2.30E-08	-0.55432	DNAJB2
59	M84443	1.37E-05	4.08E-07	4.08E-07	0.303567	GALK2
60	U32324	1.37E-05	4.08E-07	3.21E-08	0.334966	IL11RA
61	AB011115	1.37E-05	4.08E-07	3.39E-07	0.382809	KIAA0543
62	AB014535	1.37E-05	4.08E-07	1.04E-06	0.285282	KIAA0635
63	X02152	1.37E-05	4.08E-07	4.63E-08	-0.75601	LDHA
64	AF007130	2.11E-06	4.08E-07	2.51E-06	0.391811	LOC54104
65	AF007151	1.37E-05	4.08E-07	3.25E-06	0.468343	MMS19L
66	X82209	2.11E-06	4.08E-07	1.37E-09	-0.45281	MN1
67	X79882	1.37E-05	4.08E-07	1.78E-07	0.520965	MVP
68	U91616	1.37E-05	4.08E-07	1.27E-07	-0.80419	NFKBIE
69	U41815	1.37E-05	4.08E-07	2.16E-07	-0.96931	NUP98
70	AB011108	1.37E-05	4.08E-07	4.39E-07	0.453498	PRP4
71	L40377	1.37E-05	4.08E-07	3.49E-07	-0.79409	SERPINB8
72	X99656	1.37E-05	4.08E-07	1.68E-06	-0.23553	SH3GL1
73	AJ010059	2.11E-06	4.08E-07	2.95E-06	0.2235	SIT
74	J02973	1.37E-05	4.08E-07	2.93E-07	-1.30804	THBD
75	N90862	1.37E-05	4.08E-07	3.28E-08	0.43576	VAMP8
76	Y14768	1.37E-05	4.08E-07	7.26E-08	0.248383	
77	U47414	2.11E-06	7.73E-07	2.31E-06	0.370736	CCNG2
78	AB002386	2.11E-06	7.73E-07	5.34E-09	0.586117	EZH1
79	U29344	2.11E-06	7.73E-07	2.35E-07	-0.43842	FASN
80	AF015553	2.11E-06	7.73E-07	2.61E-07	0.61214	GTF2I
81	AB028981	2.11E-06	7.73E-07	5.34E-07	0.282288	KIAA1058
82	U29656	2.11E-06	7.73E-07	7.52E-08	0.353186	NME3
83	X00737	2.11E-06	7.73E-07	5.21E-08	-0.67074	NP
84	U29185	2.11E-06	7.73E-07	1.56E-07	-1.08006	PRNP
85	AB007960	2.11E-06	7.73E-07	7.96E-06	0.447772	SH3GLB1
86	U44839	2.11E-06	7.73E-07	2.54E-07	-0.97008	USP11
87	U84007	7.44E-05	1.28E-06	0.000235	0.236422	AGL

88	S78187	7.44E-05	1.28E-06	1.95E-05	0.203265	CDC25B
89	X82153	7.44E-05	1.28E-06	2.27E-06	0.47844	CTSK
90	AL050084	7.44E-05	1.28E-06	5.26E-05	0.509331	DC8
91	X62535	1.37E-05	1.28E-06	5.68E-07	0.243937	DGKA
92	AB026436	7.44E-05	1.28E-06	0.000219	-0.7589	DUSP10
93	M98833	7.44E-05	1.28E-06	1.52E-06	0.434288	FLI1
94	AW051579	1.37E-05	1.28E-06	7.58E-07	0.593476	FLJ10512
95	X16706	7.44E-05	1.28E-06	1.23E-06	-1.09747	FOSL2
96	U90917	1.37E-05	1.28E-06	3.89E-07	0.433406	FOXM1
97	M24194	7.44E-05	1.28E-06	4.38E-06	0.560895	GNB2L1
98	AJ002190	7.44E-05	1.28E-06	2.17E-08	0.33775	GNPAT
99	X87949	7.44E-05	1.28E-06	4.05E-07	-0.54468	HSPA5
100	U96876	7.44E-05	1.28E-06	3.54E-06	-0.45317	INSIG1
101	AF038564	1.37E-05	1.28E-06	2.05E-07	-0.40446	ITCH
102	D80011	7.44E-05	1.28E-06	4.20E-07	-0.35073	KIAA0189
103	AI950382	1.37E-05	1.28E-06	1.63E-07	-0.74128	KIAA0585
104	AB023235	7.44E-05	1.28E-06	1.43E-05	0.311216	KIAA1018
105	AB029038	7.44E-05	1.28E-06	7.62E-05	0.364386	KIAA1115
106	U24166	7.44E-05	1.28E-06	7.52E-06	-0.45293	MAPRE1
107	X61498	7.44E-05	1.28E-06	8.80E-07	-0.49884	NFKB2
108	U12767	7.44E-05	1.28E-06	2.84E-07	-1.23483	NR4A3
109	U85245	7.44E-05	1.28E-06	4.57E-07	0.365266	PIP5K2B
110	U50928	7.44E-05	1.28E-06	4.72E-06	0.302213	PKD2
111	U13695	7.44E-05	1.28E-06	1.11E-05	0.805607	PMS1
112	AA203527	1.37E-05	1.28E-06	1.18E-07	0.281992	RPP20
113	J02939	7.44E-05	1.28E-06	2.16E-07	-0.87844	SLC3A2
114	N30151	7.44E-05	1.28E-06	5.05E-05	0.393521	STX16
115	U52960	2.11E-06	1.28E-06	1.51E-07	-0.84863	SURB7
116	AF030249	1.37E-05	1.28E-06	1.98E-07	0.534547	
117	AL022398	7.44E-05	1.28E-06	8.09E-08	0.919627	
118	HG1103-HT1103	1.37E-05	1.28E-06	1.16E-07	-0.39165	
119	D30758	2.11E-06	1.80E-06	1.58E-05	0.27738	CENTB1
120	U75968	2.11E-06	1.80E-06	4.36E-06	0.139542	DDX11
121	M69199	2.11E-06	1.80E-06	1.45E-07	-1.9021	G0S2
122	U20982	2.11E-06	1.80E-06	1.20E-08	-0.67125	IGFBP4
123	AF040707	2.11E-06	1.80E-06	3.57E-07	0.289845	NPR2L
124	AB007927	2.11E-06	1.80E-06	2.12E-07	0.323787	RERE
125	AA902713	2.11E-06	1.80E-06	1.44E-06	0.474378	
126	U66063	2.11E-06	2.24E-06	4.70E-07	0.277185	CAMK2G
127	D13891	2.11E-06	2.24E-06	4.57E-05	-0.20577	ID2
128	AL050087	2.11E-06	2.24E-06	1.27E-07	-0.31279	KIAA1785
129	N23137	2.11E-06	2.24E-06	2.06E-07	0.247311	MPHOSPH9
130	N42007	2.11E-06	2.24E-06	9.19E-05	0.167986	NUP50
131	M74525	2.11E-06	2.24E-06	3.50E-07	-0.61792	UBE2B
132	AF035281	2.11E-06	2.24E-06	4.87E-07	0.472445	
133	U11732	1.37E-05	3.17E-06	3.04E-07	-0.22574	ETV6

134	AB002348	1.37E-05	3.17E-06	2.49E-07	0.576346	KIAA0350
135	AB007891	1.37E-05	3.17E-06	3.99E-05	0.196376	KIAA0431
136	AI754391	1.37E-05	3.17E-06	1.72E-06	-0.27657	KLF12
137	D50406	1.37E-05	3.17E-06	2.65E-05	0.461907	RECK
138	AF070617	1.37E-05	3.17E-06	3.23E-07	0.323494	
139	M23114	2.11E-06	4.08E-06	1.59E-07	-0.96141	ATP2A2
140	AF014958	2.11E-06	4.08E-06	1.05E-07	-0.42152	CCRL2
141	AF067853	1.37E-05	4.31E-06	5.02E-06	0.361707	ADSL
142	M73547	1.37E-05	4.31E-06	9.20E-08	0.438897	D5S346
143	W28319	1.37E-05	4.31E-06	1.50E-05	0.294631	FBLN1
144	AB007895	1.37E-05	4.31E-06	9.61E-07	0.186643	KIAA0435
145	AB014579	1.37E-05	4.31E-06	6.08E-08	0.367966	MGEA5
146	AF019083	1.37E-05	4.31E-06	8.34E-07	0.17011	PTENP1
147	AL080141	1.37E-05	4.31E-06	2.42E-07	0.330868	SEC31B-1
148	AF110377	1.37E-05	4.31E-06	3.05E-05	0.361232	TRRAP
149	AB002448	1.37E-05	4.31E-06	2.45E-07	0.468926	
150	AL049787	1.37E-05	4.31E-06	7.11E-06	0.311278	
151	U50527	1.37E-05	4.31E-06	5.11E-06	0.416543	
152	Z32860	1.37E-05	4.31E-06	7.81E-06	0.133192	
153	AF094481	1.37E-05	5.01E-06	2.74E-07	-0.29045	CGGBP1
154	U29171	1.37E-05	5.01E-06	1.10E-06	-0.6032	CSNK1D
155	AL050196	1.37E-05	5.01E-06	2.00E-05	-0.24688	DKFZP586D2223
156	U48807	1.37E-05	5.01E-06	4.97E-08	-0.93178	DUSP4
157	U15552	1.37E-05	5.01E-06	1.67E-05	-0.68094	HSU15552
158	L13740	1.37E-05	5.01E-06	9.10E-08	-0.61928	NR4A1
159	AF010309	1.37E-05	5.01E-06	7.36E-07	-0.28533	PIG3
160	Y18004	1.37E-05	5.01E-06	4.19E-07	-0.9465	SCML2
161	R90942	1.37E-05	5.01E-06	1.05E-05	-0.17696	ST6GALNACIV
162	W28612	1.37E-05	5.01E-06	1.70E-06	-0.25519	
163	X64330	7.44E-05	6.03E-06	2.27E-06	0.297851	ACLY
164	U49844	7.44E-05	6.03E-06	3.67E-07	0.47168	ATR
165	AB015019	7.44E-05	6.03E-06	2.75E-07	-0.24515	BAIAP2
166	AF006513	0.000344	6.03E-06	4.48E-05	-1.45973	CHD1
167	U56998	0.000344	6.03E-06	3.70E-06	-0.74294	CNK
168	S68134	0.000344	6.03E-06	8.37E-07	-1.64652	CREM
169	S68134	0.000344	6.03E-06	4.35E-06	-2.47105	CREM
170	S68271	0.000344	6.03E-06	3.03E-06	-2.07185	CREM
171	AF021819	0.000344	6.03E-06	4.41E-05	0.298771	DJ-1
172	AF029777	1.37E-05	6.03E-06	8.27E-07	0.290159	GCN5L2
173	U28811	0.000344	6.03E-06	1.33E-06	0.32855	GLG1
174	S81914	0.000344	6.03E-06	4.18E-07	-1.59146	IER3
175	X80821	0.000344	6.03E-06	8.51E-05	-0.5606	KIAA0874
176	L06895	7.44E-05	6.03E-06	1.12E-05	-0.1928	MAD
177	D78579	1.37E-05	6.03E-06	4.25E-07	-1.65638	NR4A3
178	D78579	7.44E-05	6.03E-06	9.62E-07	-1.61438	NR4A3

179	U12767	0.000344	6.03E-06	2.55E-07	-2.13744	NR4A3
180	M95678	0.000344	6.03E-06	2.00E-06	0.432923	PLCB2
181	X51804	0.000344	6.03E-06	7.23E-05	-0.19283	PMI
182	W28743	0.000344	6.03E-06	2.78E-06	-0.28926	PP1628
183	X17042	7.44E-05	6.03E-06	6.64E-06	-0.36481	PRG1
184	M80244	0.000344	6.03E-06	2.72E-06	-0.8522	SLC7A5
185	AF001294	1.37E-05	6.03E-06	1.23E-06	-0.76359	TSSC3
186	D49677	7.44E-05	6.03E-06	4.18E-06	0.198707	U2AF1RS2
187	AB011004	0.000344	6.03E-06	1.41E-06	-1.34073	UAP1
188	AB011113	1.37E-05	6.03E-06	3.74E-07	0.444795	WDR7
189	AC002394	0.000344	6.03E-06	0.001473	0.17105	
190	AL021707	0.000344	6.03E-06	4.95E-06	-2.21462	
191	AL022398	7.44E-05	6.03E-06	1.10E-07	0.79713	
192	AL049442	0.000344	6.03E-06	8.09E-06	0.621935	
193	U17760	0.000344	6.03E-06	4.25E-06	-0.84472	
194	L22569	1.37E-05	8.66E-06	1.52E-06	0.318129	CTSB
195	AL031058	1.37E-05	8.66E-06	0.000375	0.149046	DSP
196	AL080172	1.37E-05	8.66E-06	1.89E-05	0.098968	FLJ21919
197	M36821	1.37E-05	8.66E-06	2.21E-07	-0.36334	GRO3
198	U06631	1.37E-05	8.66E-06	1.31E-05	0.486332	H326
199	L16499	1.37E-05	8.66E-06	5.12E-06	0.374296	HHEX
200	X53586	1.37E-05	8.66E-06	3.40E-07	0.51291	ITGA6
201	D87466	1.37E-05	8.66E-06	1.49E-07	0.466046	KIAA0276
202	N98667	1.37E-05	8.66E-06	3.38E-07	0.367127	KIAA1696
203	X99142	1.37E-05	8.66E-06	1.24E-06	-0.29773	KRTHB6
204	AF011333	1.37E-05	8.66E-06	1.55E-05	0.342503	LY75
205	U70735	1.37E-05	8.66E-06	1.82E-06	0.249185	MOV34-34KD
206	U02020	1.37E-05	8.66E-06	1.37E-06	-1.13863	PBEF
207	M31724	1.37E-05	8.66E-06	0.000172	-0.2601	PTPN1
208	U29175	1.37E-05	8.66E-06	1.90E-06	0.266342	SMARCA4
209	AL031846	1.37E-05	8.66E-06	0.000418	0.38404	
210	Y12059	7.44E-05	1.51E-05	5.64E-06	-0.46008	BRD4
211	U49187	7.44E-05	1.51E-05	1.48E-06	0.671467	C6orf32
212	X66945	7.44E-05	1.51E-05	1.91E-07	-0.35494	FGFR1
213	M60922	7.44E-05	1.51E-05	4.47E-08	0.39657	FLOT2
214	AL049409	7.44E-05	1.51E-05	1.10E-06	0.714173	LEF1
215	L16794	7.44E-05	1.51E-05	2.23E-05	-0.27553	MEF2D
216	U77735	7.44E-05	1.51E-05	5.66E-06	0.574142	PIM2
217	U10117	7.44E-05	1.51E-05	4.07E-06	0.563673	SCYE1
218	AF023614	1.37E-05	1.51E-05	4.79E-07	-0.20744	TACI
219	S73591	1.37E-05	1.51E-05	4.68E-06	0.414777	VDUP1
220	AF052160	7.44E-05	1.51E-05	1.67E-06	0.623021	
221	L76528	7.44E-05	1.51E-05	6.14E-06	-0.39652	
222	U51007	7.44E-05	1.51E-05	1.49E-06	0.309996	
223	D10704	1.37E-05	1.75E-05	4.69E-07	-0.36791	CHK
224	U97105	1.37E-05	1.75E-05	6.56E-07	1.00615	DPYSL2

225	U03634	1.37E-05	1.75E-05	1.00E-06	-0.21467	LBC
226	L13773	1.37E-05	1.75E-05	6.44E-07	0.247919	MLLT2
227	M31523	1.37E-05	1.75E-05	2.09E-06	0.36898	TCF3
228	AL023553	1.37E-05	1.75E-05	2.51E-06	0.226635	
229	W25984	7.44E-05	2.35E-05	1.42E-05	0.482493	ACTA1
230	U78521	0.000344	2.35E-05	2.53E-05	0.320909	AIP
231	M30704	0.000344	2.35E-05	1.65E-05	-0.37795	AREG
232	X91504	0.001377	2.35E-05	0.00016	0.233217	ARFRP1
233	U51478	7.44E-05	2.35E-05	6.10E-07	-0.58	ATP1B3
234	U21551	0.001377	2.35E-05	7.60E-05	-0.3088	BCAT1
235	AB004066	0.000344	2.35E-05	6.57E-05	-0.60905	BHLHB2
236	M59040	0.001377	2.35E-05	2.82E-06	-0.46271	CD44
237	M91670	0.001377	2.35E-05	0.001649	-0.47538	E2-EPF
238	U43774	0.000344	2.35E-05	8.80E-07	-0.39938	FCAR
239	AW024285	0.000344	2.35E-05	6.99E-06	-0.42098	FLJ12443
240	AA780049	7.44E-05	2.35E-05	7.39E-07	0.54912	FLJ21439
241	AI935146	0.000344	2.35E-05	2.05E-06	-0.46726	GALNT3
242	AJ011679	0.001377	2.35E-05	4.67E-05	0.243248	GAPCENA
243	AI670100	7.44E-05	2.35E-05	7.70E-07	0.22677	GRLF1
244	D87119	7.44E-05	2.35E-05	1.80E-06	0.425625	GS3955
245	M92432	0.000344	2.35E-05	4.31E-05	0.363033	GUCY2D
246	D50405	0.001377	2.35E-05	0.000688	0.387926	HDAC1
247	U07563	7.44E-05	2.35E-05	4.91E-07	-0.25016	HSABLGR3
248	Y10313	0.001377	2.35E-05	0.003201	-0.35345	IFRD1
249	D63485	0.000344	2.35E-05	9.04E-05	0.31177	IKKE
250	L08488	0.000344	2.35E-05	7.54E-06	-0.37883	INPP1
251	X06256	1.37E-05	2.35E-05	4.89E-07	-0.7357	ITGA5
252	D42084	0.001377	2.35E-05	7.39E-06	0.222195	KIAA0094
253	D43947	7.44E-05	2.35E-05	0.000104	0.269941	KIAA0100
254	AB007870	0.000344	2.35E-05	0.000108	-0.64362	KIAA0410
255	AI950382	0.000344	2.35E-05	0.000122	-0.65985	KIAA0585
256	AB014548	7.44E-05	2.35E-05	2.77E-05	0.431229	KIAA0648
257	AB018297	0.001377	2.35E-05	0.000836	0.195704	KIAA0754
258	AI970189	0.000344	2.35E-05	6.16E-07	-0.75934	KIAA0997
259	L04733	0.001377	2.35E-05	8.84E-07	0.306455	KNS2
260	AF010193	7.44E-05	2.35E-05	1.26E-07	-1.4705	MADH7
261	U18919	7.44E-05	2.35E-05	1.05E-05	0.271231	NBP
262	U85430	0.001377	2.35E-05	0.000315	0.317554	NFATC3
263	S76638	7.44E-05	2.35E-05	7.47E-07	-0.35416	NFKB2
264	AL050353	0.000344	2.35E-05	4.42E-06	0.179352	OIP2
265	L20971	0.001377	2.35E-05	0.00089	-0.49725	PDE4B
266	AF060502	7.44E-05	2.35E-05	0.000114	-0.18239	PEX10
267	X80497	0.001377	2.35E-05	0.000245	0.313262	PHKA2
268	AL050371	0.000344	2.35E-05	3.70E-06	0.493288	PISD
269	U77718	7.44E-05	2.35E-05	6.60E-06	0.352996	PNN
270	U52427	0.001377	2.35E-05	0.000282	0.329478	POLR2G

271	U94778	0.000344	2.35E-05	1.18E-05	0.282929	PSTPIP1
272	U48296	0.001377	2.35E-05	0.00011	-0.89871	PTP4A1
273	M31166	0.001377	2.35E-05	0.000256	-0.38484	PTX3
274	AJ001016	7.44E-05	2.35E-05	1.08E-05	-0.28245	RAMP3
275	AF040965	0.001377	2.35E-05	0.001101	-0.38591	RES4-25
276	J04130	0.000344	2.35E-05	3.02E-06	-0.62071	SCYA4
277	U81800	0.000344	2.35E-05	4.28E-05	-0.49523	SLC16A3
278	AB000734	0.001377	2.35E-05	0.000883	-0.58764	SSI-1
279	U38847	7.44E-05	2.35E-05	9.91E-07	0.222946	TARBP1
280	M63180	0.001377	2.35E-05	1.03E-05	-0.33301	TARS
281	D15050	0.001377	2.35E-05	0.000192	-1.12874	TCF8
282	M12959	7.44E-05	2.35E-05	1.61E-06	0.128482	TRA@
283	X00734	0.001377	2.35E-05	0.000384	-0.34516	TUBB5
284	AJ001340	0.001377	2.35E-05	4.21E-05	0.181208	U3-55K
285	Y08614	0.001377	2.35E-05	6.92E-05	0.305659	XPO1
286	AF054589	0.000344	2.35E-05	1.98E-06	0.945394	
287	AL022398	7.44E-05	2.35E-05	2.40E-06	0.493166	
288	AL031178	7.44E-05	2.35E-05	3.18E-05	0.410068	
289	AL049782	7.44E-05	2.35E-05	7.66E-07	0.237794	
290	HG1471-HT3923	0.001377	2.35E-05	0.000519	0.203133	
291	HG4582-HT4987	7.44E-05	2.35E-05	4.63E-07	-0.39588	
292	U96629	0.001377	2.35E-05	1.00E-04	0.277256	
293	D64110	7.44E-05	2.58E-05	7.49E-05	-0.51036	BTG3
294	J04111	7.44E-05	2.58E-05	0.000108	-1.60276	JUN
295	J04111	7.44E-05	2.58E-05	4.68E-05	-1.14014	JUN
296	X56681	7.44E-05	2.58E-05	0.000112	-0.48711	JUND
297	D21853	7.44E-05	2.58E-05	0.000403	-0.25594	KIAA0111
298	X80692	7.44E-05	2.58E-05	3.44E-05	-1.1939	MAPK6
299	S76638	7.44E-05	2.58E-05	5.23E-05	-0.46026	NFKB2
300	U65785	7.44E-05	2.58E-05	9.67E-06	-0.2389	ORP150
301	AB016247	7.44E-05	2.58E-05	3.13E-05	-0.57287	SC5DL
302	M55153	7.44E-05	2.58E-05	4.77E-06	-0.27465	TGM2
303	U02570	1.37E-05	2.81E-05	1.26E-06	0.432431	ARHGAP1
304	X04366	1.37E-05	2.81E-05	5.11E-06	0.346076	CAPN1
305	L10413	1.37E-05	2.81E-05	6.46E-06	0.207231	FNTA
306	AF055001	1.37E-05	2.81E-05	9.78E-06	-0.9457	HERPUD1
307	AI523538	1.37E-05	2.81E-05	0.004471	-0.1584	HIPK3
308	X59373	1.37E-05	2.81E-05	1.31E-05	-0.22992	HOXD10
309	X99209	1.37E-05	2.81E-05	2.65E-05	0.239777	HRMT1L1
310	M65217	1.37E-05	2.81E-05	1.02E-05	0.33377	HSF2
311	X17025	1.37E-05	2.81E-05	1.45E-05	-0.44351	IDI1
312	M35878	1.37E-05	2.81E-05	4.29E-05	-0.25267	IGFBP3
313	D63486	1.37E-05	2.81E-05	9.69E-06	0.235319	KIAA0152
314	AB002303	1.37E-05	2.81E-05	1.86E-05	-0.39642	KIAA0305
315	U20816	1.37E-05	2.81E-05	4.92E-05	-0.20145	NFKB2
316	M61906	1.37E-05	2.81E-05	5.93E-06	-0.39875	PIK3R1

317	U13695	1.37E-05	2.81E-05	1.31E-05	0.362255	PMS1
318	U38979	1.37E-05	2.81E-05	3.95E-05	0.158105	PMS2L9
319	X70218	1.37E-05	2.81E-05	2.44E-06	-0.74691	PPP4C
320	AC002400	1.37E-05	2.81E-05	2.28E-06	-0.25834	
321	AC005390	1.37E-05	2.81E-05	2.99E-05	-0.24231	
322	AF070606	1.37E-05	2.81E-05	1.48E-06	-0.89337	
323	HG2724-HT2820	1.37E-05	2.81E-05	5.17E-06	-1.33814	
324	X84194	7.44E-05	4.67E-05	6.38E-05	0.23578	ACYP1
325	AF039656	0.00482	4.67E-05	0.000251	-0.73273	BASP1
326	AB002384	0.00482	4.67E-05	4.22E-05	0.548091	C6orf32
327	X98172	7.44E-05	4.67E-05	5.29E-07	0.507556	CASP8
328	U60521	7.44E-05	4.67E-05	8.13E-06	-0.36762	CASP9
329	U11791	0.00482	4.67E-05	0.000363	-1.0232	CCNH
330	U67615	0.00482	4.67E-05	0.000948	1.23433	CHS1
331	AF037339	0.000344	4.67E-05	1.59E-05	-0.33549	CLPTM1
332	U65928	7.44E-05	4.67E-05	2.85E-07	0.408918	COPS5
333	U37408	7.44E-05	4.67E-05	3.06E-05	0.157458	CTBP1
334	AB023143	0.00482	4.67E-05	0.001982	0.215415	DEFCAP
335	AB014888	0.001377	4.67E-05	0.000204	-0.34841	DNAJB6
336	M60278	0.00482	4.67E-05	3.33E-05	-0.9007	DTR
337	U88629	0.000344	4.67E-05	9.58E-07	-0.32607	ELL2
338	M31899	0.000344	4.67E-05	0.000339	0.274507	ERCC3
339	M94856	7.44E-05	4.67E-05	4.99E-06	-0.23847	FABP5
340	X86779	0.001377	4.67E-05	1.08E-05	0.140032	FASTK
341	L00634	0.00482	4.67E-05	0.00019	0.205256	FNTA
342	AF078077	0.000344	4.67E-05	1.44E-05	-1.47649	GADD45B
343	D87119	7.44E-05	4.67E-05	4.62E-06	0.557116	GS3955
344	X17644	7.44E-05	4.67E-05	6.72E-06	-0.71963	GSPT1
345	L19314	0.00482	4.67E-05	0.000922	-0.35113	HRY
346	U05681	7.44E-05	4.67E-05	3.37E-06	-0.35383	HSBCL3S2
347	J00139	0.00482	4.67E-05	0.000196	-0.12797	HUMFOL5
348	M24283	0.000344	4.67E-05	3.71E-06	-1.32611	ICAM1
349	M62403	7.44E-05	4.67E-05	5.57E-07	-0.53749	IGFBP4
350	M28130	7.44E-05	4.67E-05	8.02E-07	-2.27292	IL8
351	Z56281	0.001377	4.67E-05	0.000243	0.309173	IRF3
352	L12002	7.44E-05	4.67E-05	1.23E-06	0.286717	ITGA4
353	K00558	0.001377	4.67E-05	0.002498	0.12909	K-ALPHA-1
354	AL044599	0.001377	4.67E-05	8.81E-05	0.321294	KIAA0222
355	AB002344	0.000344	4.67E-05	1.04E-05	-0.39307	KIAA0346
356	AB007889	7.44E-05	4.67E-05	2.33E-05	0.255643	KIAA0429
357	AB007916	0.00482	4.67E-05	0.000147	0.493018	KIAA0447
358	AB014538	0.000344	4.67E-05	1.98E-06	-0.63923	KIAA0638
359	AF055004	7.44E-05	4.67E-05	9.29E-05	0.200537	KIAA0763
360	AI148772	0.000344	4.67E-05	4.18E-06	-1.02619	KYNU
361	AF064491	0.00482	4.67E-05	0.000148	-0.54215	LDB1
362	L78132	7.44E-05	4.67E-05	5.15E-07	0.358576	LGALS8

363	X83441	7.44E-05	4.67E-05	6.75E-06	-0.17796	LIG4
364	AF055581	7.44E-05	4.67E-05	5.69E-06	-1.05728	LNK
365	AL049963	0.000344	4.67E-05	8.36E-07	-0.74421	LOC64116
366	AF014837	0.00482	4.67E-05	0.000636	0.325349	M6A
367	D14497	0.001377	4.67E-05	3.68E-05	-0.58619	MAP3K8
368	X75346	7.44E-05	4.67E-05	1.99E-05	-0.37877	MAPKAPK2
369	M62324	0.001377	4.67E-05	5.46E-05	-0.44552	MRF-1
370	AB023208	0.000344	4.67E-05	1.37E-05	0.293901	MSF
371	AF072928	0.001377	4.67E-05	1.13E-05	-0.3089	MTMR6
372	AF045451	0.000344	4.67E-05	6.34E-06	-0.40149	NAB1
373	M58603	7.44E-05	4.67E-05	1.28E-06	-0.73537	NFKB1
374	U07132	0.00482	4.67E-05	0.001821	-0.14679	NR1H2
375	X75918	7.44E-05	4.67E-05	3.50E-05	-1.61126	NR4A2
376	S77154	0.00482	4.67E-05	0.000304	-1.33785	NR4A2
377	AB020657	0.00482	4.67E-05	2.75E-05	-0.50544	NS1-BP
378	D88674	7.44E-05	4.67E-05	6.26E-06	-0.99818	OAZIN
379	U27459	0.00482	4.67E-05	3.39E-05	0.430016	ORC2L
380	AF000545	7.44E-05	4.67E-05	3.48E-06	-0.85393	P2Y10
381	AF005043	7.44E-05	4.67E-05	2.70E-06	0.408592	PARG
382	AF026086	0.000344	4.67E-05	2.66E-06	0.297942	PEX1
383	AJ001625	7.44E-05	4.67E-05	9.91E-05	0.36837	PEX3
384	U30255	0.001377	4.67E-05	0.000826	0.325906	PGD
385	M61906	0.000344	4.67E-05	0.000611	-0.2492	PIK3R1
386	M60483	0.000344	4.67E-05	3.17E-05	-0.32565	PPP2CA
387	U14603	7.44E-05	4.67E-05	4.46E-05	0.427268	PTP4A2
388	AF069517	0.001377	4.67E-05	0.000441	0.330897	RBM6
389	M83221	0.000344	4.67E-05	1.58E-05	-0.26782	RELB
390	AF037195	0.00482	4.67E-05	8.27E-05	0.959619	RGS14
391	L07597	0.00482	4.67E-05	0.000169	0.277243	RPS6KA1
392	X15217	7.44E-05	4.67E-05	3.77E-07	-0.2371	SKIL
393	M20681	0.001377	4.67E-05	1.92E-05	-0.99917	SLC2A3
394	AF030409	7.44E-05	4.67E-05	7.66E-06	0.412043	SLC9A6
395	AJ224358	0.00482	4.67E-05	0.009613	0.14432	SURF5
396	U49928	0.000344	4.67E-05	6.31E-06	0.352648	TAB1
397	X89750	7.44E-05	4.67E-05	7.38E-06	-1.51687	TGIF
398	AA453183	0.001377	4.67E-05	4.48E-05	-0.61646	TIM17
399	M31165	7.44E-05	4.67E-05	1.38E-06	-0.34617	TNFAIP6
400	AF064090	0.001377	4.67E-05	4.05E-05	-0.38921	TNFSF14
401	AF082557	0.001377	4.67E-05	2.23E-06	0.226994	TNKS
402	D87448	0.00482	4.67E-05	0.000735	0.468196	TOPBP1
403	X05276	0.00482	4.67E-05	8.97E-05	-0.50457	TPM4
404	D50919	0.00482	4.67E-05	4.02E-05	0.332326	TRIM14
405	J03258	0.00482	4.67E-05	8.78E-05	-0.33021	VDR
406	AB007973	0.00482	4.67E-05	0.000146	0.271053	
407	AF041081	0.00482	4.67E-05	5.92E-05	0.26539	
408	AI889718	7.44E-05	4.67E-05	0.000143	-0.15002	

409	AL021154	0.000344	4.67E-05	2.19E-06	-0.82935	
410	AL049340	0.000344	4.67E-05	4.87E-05	-0.91769	
411	AL050078	0.000344	4.67E-05	1.63E-05	-0.2875	
412	AL050378	0.000344	4.67E-05	5.72E-06	0.360577	
413	D50525	0.000344	4.67E-05	3.02E-06	0.486698	
414	J04755	7.44E-05	4.67E-05	6.75E-05	-0.37296	
415	M60784	7.44E-05	4.67E-05	1.24E-06	0.559903	
416	M63978	0.000344	4.67E-05	1.77E-06	-0.44762	
417	U90909	0.00482	4.67E-05	3.74E-05	-0.64272	
418	X63547	0.001377	4.67E-05	0.000303	0.505712	
419	AA135683	0.000344	5.23E-05	0.000289	-0.69258	BASP1
420	S78771	0.000344	5.23E-05	2.55E-06	-0.31389	BRD2
421	AL080156	0.000344	5.23E-05	3.52E-05	-0.94419	DKFZP434J214
422	D14838	0.000344	5.23E-05	7.34E-06	-0.50648	FGF9
423	W28281	0.000344	5.23E-05	8.96E-06	-1.09149	GABARAPL1
424	AB002344	7.44E-05	5.23E-05	8.48E-07	-1.00068	KIAA0346
425	U23070	0.000344	5.23E-05	3.62E-05	-0.12321	NMA
426	U04636	0.000344	5.23E-05	2.81E-06	-1.85123	PTGS2
427	U47634	0.000344	5.23E-05	0.002405	-0.21686	TUBB4
428	S73149	0.000344	5.23E-05	0.003714	-0.15741	
429	M63256	0.000344	5.92E-05	6.54E-07	0.454561	CDR2
430	U94905	0.000344	5.92E-05	2.08E-05	0.388608	DGKZ
431	AF012023	7.44E-05	5.92E-05	1.02E-06	0.50623	ICAP-1A
432	L10717	0.000344	5.92E-05	0.000158	0.345558	ITK
433	D29642	0.000344	5.92E-05	8.30E-06	0.327019	KIAA0053
434	AB011128	0.000344	5.92E-05	0.000584	0.151161	KIAA0556
435	AF075587	0.000344	5.92E-05	7.55E-06	0.4405	KIAA0916
436	U66464	0.000344	5.92E-05	2.93E-05	0.255675	MAP4K1
437	U18919	0.000344	5.92E-05	0.000573	0.277847	NBP
438	X58965	0.000344	5.92E-05	7.34E-05	0.231912	NME2
439	X13403	7.44E-05	5.92E-05	4.21E-07	0.146032	POU2F1
440	D89859	0.000344	5.92E-05	1.56E-05	0.375402	ZFP161
441	AF052100	0.000344	5.92E-05	1.37E-05	0.290021	
442	N53547	7.44E-05	7.24E-05	1.80E-07	0.296678	MGC5508
443	L35013	0.000344	7.24E-05	0.000112	-0.17331	SF3B4
444	Y17829	7.44E-05	7.24E-05	5.49E-06	-0.6508	SYN47
445	AL049987	7.44E-05	7.24E-05	2.39E-05	0.193082	
446	X66436	0.000344	7.24E-05	1.88E-06	-0.26662	
447	Z80345	7.44E-05	9.64E-05	7.31E-06	0.412137	ACADS
448	U27467	7.44E-05	9.64E-05	5.65E-06	-0.56637	BCL2A1
449	AI961669	7.44E-05	9.64E-05	0.000107	-0.1656	BIG2
450	X61123	7.44E-05	9.64E-05	4.17E-07	-1.15256	BTG1
451	U49187	7.44E-05	9.64E-05	3.53E-06	0.511392	C6orf32
452	D13639	7.44E-05	9.64E-05	8.56E-06	-0.64255	CCND2
453	AL035398	7.44E-05	9.64E-05	0.000153	0.353395	CGI-51
454	U15932	7.44E-05	9.64E-05	0.00031	-1.26603	DUSP5

455	AD001530	7.44E-05	9.64E-05	3.06E-05	-0.37019	DXS9928E
456	Y07909	7.44E-05	9.64E-05	0.000161	-0.23489	EMP1
457	W27152	7.44E-05	9.64E-05	0.000502	0.186359	FLJ10569
458	L17131	7.44E-05	9.64E-05	1.48E-05	-0.24039	HMGIY
459	X04430	7.44E-05	9.64E-05	4.15E-05	-0.21816	IL6
460	AB014608	7.44E-05	9.64E-05	4.59E-06	0.41494	KIAA0708
461	AF061258	7.44E-05	9.64E-05	1.58E-06	0.622201	LIM
462	U90919	7.44E-05	9.64E-05	7.23E-06	-0.50014	LOC57862
463	J05037	7.44E-05	9.64E-05	0.000185	-0.19243	SDS
464	X70944	7.44E-05	9.64E-05	2.08E-05	-0.72892	SFPQ
465	L41887	7.44E-05	9.64E-05	6.74E-06	-0.52203	SFRS7
466	X59871	7.44E-05	9.64E-05	1.91E-05	0.376648	TCF7
467	AI742846	7.44E-05	9.64E-05	0.000374	-0.48069	VAPA
468	HG2007-HT2056	7.44E-05	9.64E-05	4.01E-06	-0.41408	
469	X58141	7.44E-05	9.64E-05	1.75E-06	0.384254	
470	AB018323	7.44E-05	0.000106	2.41E-05	0.432301	GASC1
471	AB023192	7.44E-05	0.000106	0.000138	0.196185	I-1
472	AB020638	7.44E-05	0.000106	5.26E-05	0.233629	KIAA0831
473	U49395	7.44E-05	0.000106	0.001916	0.169175	P2RX5
474	M23379	7.44E-05	0.000106	3.22E-05	0.42571	RASA1
475	AF034176	7.44E-05	0.000106	0.000333	0.332105	
476	AJ012755	7.44E-05	0.000106	0.000296	0.26445	
477	AB007934	7.44E-05	0.000119	6.08E-06	0.345799	ACF7
478	M80899	7.44E-05	0.000119	2.48E-05	0.419409	AHNAK
479	AB014529	7.44E-05	0.000119	1.84E-05	0.43403	AKAP11
480	U37547	7.44E-05	0.000119	6.74E-06	-0.71736	BIRC2
481	U72649	7.44E-05	0.000119	0.000207	-0.30079	BTG2
482	D49738	7.44E-05	0.000119	0.000136	0.292742	CKAP1
483	AJ006267	7.44E-05	0.000119	7.19E-06	0.427023	CLPX
484	W28167	7.44E-05	0.000119	1.16E-05	0.214921	COPS7A
485	U18300	7.44E-05	0.000119	2.43E-06	0.183171	DDB2
486	AI133727	7.44E-05	0.000119	1.43E-06	0.181464	FLB6421
487	AA526812	7.44E-05	0.000119	0.000106	0.259476	FLJ10326
488	D64142	7.44E-05	0.000119	1.66E-05	0.528036	H1FX
489	U60319	7.44E-05	0.000119	0.001064	0.194324	HFE
490	M17017	7.44E-05	0.000119	1.43E-06	-1.74073	IL8
491	D32053	7.44E-05	0.000119	0.003279	0.222661	KARS
492	AB007914	7.44E-05	0.000119	7.13E-05	0.302838	KIAA0445
493	U10485	7.44E-05	0.000119	7.40E-06	0.270352	LRMP
494	U29656	7.44E-05	0.000119	4.31E-06	0.471876	NME3
495	AB014604	7.44E-05	0.000119	1.72E-05	0.425787	OSBPL3
496	U41745	7.44E-05	0.000119	0.00204	0.230274	PDAP1
497	S90469	7.44E-05	0.000119	5.56E-06	-0.2636	POR
498	M26683	7.44E-05	0.000119	3.70E-06	-0.16179	SCYA2
499	X81789	7.44E-05	0.000119	2.23E-05	0.143079	SF3A3
500	L14595	7.44E-05	0.000119	3.55E-05	-0.1953	SLC1A4

501	AL079286	7.44E-05	0.000119	0.000245	0.165851	STAU2
502	AA845349	7.44E-05	0.000119	7.78E-07	0.457176	TRIP7
503	X59303	7.44E-05	0.000119	0.000124	0.224891	VARS2
504	AB023219	7.44E-05	0.000119	1.41E-05	0.316475	
505	M58603	7.44E-05	0.000129	9.08E-06	-0.56835	NFKB1
506	X77723	7.44E-05	0.000129	0.006788	-0.24317	RAB5EP
507	AF117829	7.44E-05	0.000129	2.61E-06	-0.57516	RIPK2
508	U52960	7.44E-05	0.000129	0.001042	-0.24648	SURB7
509	U84011	0.00482	0.000149	0.000134	0.286331	AGL
510	U90552	0.000344	0.000149	0.000182	0.288509	BTN3A1
511	M16336	0.00482	0.000149	0.000224	0.218007	CD2
512	U03106	0.000344	0.000149	0.000252	-0.87784	CDKN1A
513	AB009285	0.001377	0.000149	0.000137	0.235726	CFDP1
514	U63289	0.001377	0.000149	0.001722	-0.43517	CUGBP1
515	AF000430	0.00482	0.000149	0.000694	-0.19887	DNM1L
516	L11329	0.001377	0.000149	0.000142	-0.56584	DUSP2
517	AB007619	0.00482	0.000149	0.002073	0.198391	EBAG9
518	X81625	0.00482	0.000149	6.92E-05	-0.80689	ETF1
519	AL050128	0.000344	0.000149	1.81E-05	0.459416	FAM8A1
520	L49169	0.001377	0.000149	8.18E-05	-2.09549	FOSB
521	L25665	0.000344	0.000149	3.34E-06	-0.4513	GNL1
522	AI494623	0.00482	0.000149	0.000304	0.187206	HCDI
523	D89678	0.001377	0.000149	3.03E-05	0.197298	HNRPDL
524	U07563	0.000344	0.000149	1.02E-05	-0.23627	HSABLGR3
525	W28589	0.00482	0.000149	0.000129	0.170457	HSPD1
526	N29665	0.000344	0.000149	3.34E-05	0.593294	KIAA0618
527	AB023207	0.000344	0.000149	8.64E-06	-0.4056	KIAA0990
528	AL079277	0.00482	0.000149	0.000161	0.200656	LOC54103
529	Z14138	0.001377	0.000149	0.000197	-0.85008	MAP3K8
530	N23137	0.001377	0.000149	4.12E-06	0.244083	MPHOSPH9
531	AF050640	0.001377	0.000149	6.03E-05	0.324021	NDUFS2
532	AF069987	0.001377	0.000149	4.44E-05	0.203382	NIT1
533	AF043325	0.000344	0.000149	1.06E-05	0.328186	NMT2
534	M10901	0.001377	0.000149	1.91E-05	-0.58982	NR3C1
535	M12267	0.000344	0.000149	4.07E-06	-0.3279	OAT
536	U02882	0.00482	0.000149	0.000223	-0.99878	PDE4D
537	AF059531	0.000344	0.000149	6.73E-06	0.546441	PRMT3
538	M29893	0.001377	0.000149	9.96E-05	-0.15688	RALA
539	AB029028	0.001377	0.000149	9.11E-06	0.482258	RAP140
540	AB007448	0.00482	0.000149	0.000777	-0.319	SLC22A4
541	D87969	0.00482	0.000149	0.001578	0.401991	SLC35A1
542	U66615	0.00482	0.000149	0.000196	0.235993	SMARCC1
543	U46691	0.00482	0.000149	1.48E-05	-0.85179	SUPT6H
544	AF049910	0.00482	0.000149	0.000373	-0.32787	TACC1
545	X14787	0.001377	0.000149	2.88E-05	-0.19161	THBS1
546	AI375913	0.00482	0.000149	0.000905	-0.12102	TOP2A

547	X02344	0.001377	0.000149	0.00414	-0.20405	TUBB2
548	AF104421	0.000344	0.000149	6.50E-06	0.349373	UROD
549	J03258	0.000344	0.000149	1.21E-06	-0.58295	VDR
550	M58297	0.000344	0.000149	1.57E-05	0.185829	ZNF42
551	Y11681	0.000344	0.000149	1.92E-05	0.234481	
552	AF104942	0.001377	0.00019	4.83E-05	0.464438	ABCC5
553	L07261	0.000344	0.00019	0.003564	0.29763	ADD1
554	L19871	0.001377	0.00019	0.000105	-0.19867	ATF3
555	J04027	0.000344	0.00019	0.000133	-0.42466	ATP2B1
556	M83363	0.001377	0.00019	0.004471	0.177565	ATP2B4
557	AF038195	0.000344	0.00019	0.000134	0.281425	BCS1L
558	S78771	0.001377	0.00019	0.000145	-0.24109	BRD2
559	L07044	0.001377	0.00019	0.000284	0.186013	CAMK2G
560	M28170	0.000344	0.00019	2.96E-05	0.356602	CD19
561	Y08682	0.000344	0.00019	0.000118	0.17398	CPT1B
562	AF046059	0.001377	0.00019	0.000665	0.204072	CREME9
563	L06797	0.001377	0.00019	0.000455	-0.93505	CXCR4
564	L39874	0.000344	0.00019	0.000354	0.353702	DCTD
565	AC004475	0.000344	0.00019	2.86E-05	0.25205	DKFZP434E2216
566	AI538172	0.001377	0.00019	0.000621	0.243057	DKFZp761B2423
567	AF010187	0.000344	0.00019	1.00E-05	0.361895	FIBP
568	AW051579	0.000344	0.00019	0.000258	0.390285	FLJ10512
569	M22632	0.001377	0.00019	1.34E-05	0.157239	GOT2
570	X59372	0.001377	0.00019	0.000528	-0.12959	HOXD9
571	X12433	0.000344	0.00019	1.07E-05	-0.39946	HS1-2
572	X15183	0.000344	0.00019	0.000645	-0.22973	HSPCA
573	AI912041	0.001377	0.00019	5.21E-05	-0.38517	HSPE1
574	X75315	0.000344	0.00019	0.010841	-0.64335	HSRNASEB
575	L42324	0.000344	0.00019	0.000262	-0.31758	HUMFRCG
576	X69433	0.001377	0.00019	0.002925	0.209735	IDH2
577	Y00093	0.000344	0.00019	2.60E-05	-0.39318	ITGAX
578	M88458	0.001377	0.00019	0.002031	-0.15998	KDELR2
579	AB011114	0.000344	0.00019	3.13E-05	0.278271	KIAA0542
580	AB011135	0.000344	0.00019	0.000149	0.247752	KIAA0563
581	U57721	0.001377	0.00019	3.47E-05	-0.23188	KYNU
582	Y11395	0.001377	0.00019	8.58E-05	0.34059	LANCL1
583	AI652660	0.000344	0.00019	2.28E-05	0.385107	LOC51112
584	AB026118	0.001377	0.00019	4.47E-06	-0.24886	MALT1
585	AB011144	0.000344	0.00019	9.36E-05	0.26851	MCM3AP
586	AI620381	0.000344	0.00019	8.06E-06	0.29605	MGC3077
587	AI525633	0.000344	0.00019	2.44E-05	0.170916	MGC5576
588	X16396	0.000344	0.00019	3.27E-06	-0.6151	MTHFD2
589	V00568	0.000344	0.00019	0.000769	0.549224	MYC
590	AL050281	0.000344	0.00019	2.85E-06	0.30517	NAG
591	AI985272	0.000344	0.00019	0.000474	-0.2571	NMB
592	D38524	0.000344	0.00019	0.001313	0.228851	NT5B

593	AJ225089	0.000344	0.00019	0.000531	-0.2589	OASL
594	Z82200	0.000344	0.00019	0.000136	-0.28579	P2Y10
595	X63564	0.001377	0.00019	1.70E-05	-0.28202	POLR2A
596	S57501	0.001377	0.00019	0.002179	0.267744	PPP1CA
597	X07109	0.000344	0.00019	0.000694	0.167774	PRKCB1
598	M28209	0.000344	0.00019	0.000392	-0.52456	RAB1
599	M87339	0.000344	0.00019	3.41E-05	0.248151	RFC4
600	Z14000	0.000344	0.00019	3.91E-06	-0.33734	RING1
601	X06815	0.000344	0.00019	3.50E-05	0.293968	SNRP70
602	L23959	0.000344	0.00019	1.82E-05	-0.36834	TFDP1
603	AB018262	0.000344	0.00019	0.000241	0.319056	TOMM70A
604	X00437	0.001377	0.00019	0.00022	0.248344	TRB@
605	AF061016	0.000344	0.00019	0.000264	0.349913	UGDH
606	U62392	0.000344	0.00019	2.74E-05	-0.65983	ZNF193
607	X78925	0.001377	0.00019	0.001253	-0.28003	ZNF267
608	AI655015	0.001377	0.00019	0.00444	0.74681	
609	AL049387	0.001377	0.00019	5.12E-06	0.379296	
610	AL050376	0.000344	0.00019	0.00026	0.410405	
611	AB008775	0.000344	0.000304	1.88E-06	-0.80745	AQP9
612	AI141670	0.000344	0.000304	1.60E-06	-0.2494	CLCN2
613	AL080071	0.000344	0.000304	3.12E-06	0.237367	DKFZP564M082
614	AB028964	0.000344	0.000304	5.07E-05	0.351352	KIAA1041
615	M16801	0.001377	0.000304	0.000458	0.412733	NR3C2
616	N36842	0.001377	0.000304	0.000577	0.172944	UPF3A
617	AL096752	0.000344	0.000304	0.000323	-0.20419	
618	U76421	0.000344	0.000402	0.000278	0.226301	ADARB1
619	L13939	0.001377	0.000402	0.000215	0.180874	AP1B1
620	X97074	0.001377	0.000402	0.001924	0.298218	AP2S1
621	U72936	0.000344	0.000402	1.03E-05	0.356824	ATRX
622	X94910	0.000344	0.000402	0.000204	0.249294	C12orf8
623	U18291	0.000344	0.000402	2.45E-05	0.594377	CDC16
624	L22005	0.001377	0.000402	0.000111	-0.15257	CDC34
625	M59287	0.00482	0.000402	0.000276	-0.72279	CLK1
626	U25435	0.000344	0.000402	0.000648	0.264876	CTCF
627	L39874	0.000344	0.000402	2.41E-05	0.211923	DCTD
628	X52104	0.000344	0.000402	0.000159	0.317963	DDX5
629	AL050062	0.000344	0.000402	0.000377	0.36401	DKFZP566K023
630	AL080081	0.00482	0.000402	0.000103	-0.60871	DNAJB9
631	X63741	0.001377	0.000402	0.000175	-0.59207	EGR3
632	D13988	0.001377	0.000402	0.000371	0.14676	GDI2
633	M27492	0.000344	0.000402	2.01E-06	-0.32619	IL1R1
634	S66213	0.000344	0.000402	9.56E-05	0.247863	ITGA6
635	AJ005896	0.000344	0.000402	5.38E-05	0.210462	JM4
636	Y10745	0.00482	0.000402	6.39E-05	-0.30524	KCNJ15
637	AB002374	0.00482	0.000402	0.000916	0.20284	KIAA0376
638	AB007874	0.001377	0.000402	0.000181	-0.21662	KIAA0414

639	AB011133	0.00482	0.000402	0.000521	0.302843	KIAA0561
640	AB018335	0.00482	0.000402	9.03E-05	0.234274	KIAA0792
641	M13452	0.00482	0.000402	0.00148	-0.28339	LMNA
642	X68836	0.00482	0.000402	2.15E-05	-0.57967	MAT2A
643	U79256	0.000344	0.000402	2.24E-05	0.328028	MGC14258
644	X76538	0.001377	0.000402	5.62E-05	0.408464	MPV17
645	AB011093	0.000344	0.000402	0.000101	0.612928	P114-RHO-GEF
646	X66363	0.001377	0.000402	6.80E-05	-0.24041	PCTK1
647	U13695	0.00482	0.000402	2.31E-05	0.31531	PMS1
648	D87078	0.000344	0.000402	3.88E-05	0.497225	PUM2
649	Z97074	0.001377	0.000402	3.97E-05	0.296662	RAB9P40
650	X90530	0.000344	0.000402	3.52E-05	0.254197	RAGB
651	U75679	0.001377	0.000402	0.000139	-0.29594	SLBP
652	AF007142	0.000344	0.000402	3.15E-06	0.678734	
653	AL021977	0.00482	0.000402	8.82E-05	-0.82538	
654	AL080192	0.001377	0.000402	4.26E-05	0.201319	
655	HG1980-HT2023	0.00482	0.000402	0.003775	-0.48359	
656	U47924	0.001377	0.000402	0.000134	0.52195	
657	U83661	0.000344	0.000444	9.97E-06	0.270218	ABCC5
658	AI961929	0.000344	0.000444	1.88E-05	0.461528	ARHGAP1
659	X78817	0.000344	0.000444	2.82E-05	0.281835	ARHGAP4
660	AL080164	0.000344	0.000444	0.000218	0.268161	DKFZP564C1940
661	X90392	0.000344	0.000444	0.000208	0.150242	DNASE1L1
662	AI561196	0.000344	0.000444	0.000156	0.302434	FLJ11806
663	AJ008112	0.000344	0.000444	0.000246	-0.32126	FMNL
664	M94630	0.000344	0.000444	0.000244	0.274532	HNRPD
665	M38180	0.000344	0.000444	0.003037	-0.15741	HSD3B1
666	U79274	0.000344	0.000444	9.67E-05	0.285563	HSU79274
667	AB014585	0.000344	0.000444	6.48E-05	0.460196	KIAA0685
668	AB029001	0.000344	0.000444	0.000183	-0.33324	KIAA1078
669	AA045160	0.000344	0.000444	4.62E-05	0.179556	MRPS14
670	M96824	0.000344	0.000444	2.18E-05	0.139326	NUCB1
671	Y10055	0.000344	0.000444	9.91E-06	0.176067	PIK3CD
672	Z54367	0.000344	0.000444	1.30E-05	-0.39738	PLEC1
673	AF014402	0.000344	0.000444	7.63E-05	0.147061	PPAP2A
674	M30773	0.000344	0.000444	0.001161	0.41229	PPP3R1
675	M29386	0.000344	0.000444	6.26E-05	-0.23554	PRL
676	X02910	0.000344	0.000444	0.001378	-0.17579	TNF
677	S76792	0.000344	0.000444	0.000211	-0.16737	TNFRSF4
678	Y09008	0.000344	0.000444	0.000352	0.168444	UNG
679	U18009	0.000344	0.000444	0.002896	0.204706	VATI
680	D14533	0.000344	0.000444	0.000837	0.246085	XPA
681	W27419	0.000344	0.000444	2.83E-05	-0.44121	
682	Z85986	0.000344	0.000444	0.000407	-0.2149	
683	Z99716	0.000344	0.000444	5.14E-05	0.324642	
684	U50939	0.001377	0.000525	1.19E-05	0.235552	APPBP1

685	Y15521	0.00482	0.000525	0.000492	-0.28889	ASMTL
686	J05682	0.00482	0.000525	0.000291	-0.33004	ATP6C
687	D26362	0.00482	0.000525	0.000707	0.247252	BRD3
688	AL120687	0.001377	0.000525	1.21E-05	-0.55731	CSH1
689	U20350	0.00482	0.000525	0.010386	0.383475	CX3CR1
690	X04011	0.00482	0.000525	0.000154	0.348439	CYBB
691	U78524	0.001377	0.000525	6.56E-05	-0.36872	DDXBP1
692	U87947	0.001377	0.000525	5.05E-05	-0.29673	EMP3
693	AL035252	0.00482	0.000525	0.003735	0.074075	ENTPD6
694	X04828	0.00482	0.000525	0.0015	0.256297	GNAI2
695	X56841	0.001377	0.000525	4.37E-05	0.338907	HLA-E
696	D49410	0.00482	0.000525	0.00016	-0.21753	HUMIL3RA12
697	L40586	0.00482	0.000525	3.02E-05	-0.20891	IDS
698	X52015	0.00482	0.000525	0.00032	-0.54051	IL1RN
699	D31888	0.00482	0.000525	7.50E-06	-0.44687	KIAA0071
700	D42047	0.001377	0.000525	3.50E-05	0.226884	KIAA0089
701	AB007958	0.00482	0.000525	0.00023	0.259725	KIAA0489
702	AB011100	0.00482	0.000525	0.000193	0.418151	KIAA0528
703	AB014553	0.00482	0.000525	0.002002	-0.25439	KIAA0653
704	AI888084	0.001377	0.000525	3.57E-05	0.391754	KIAA1624
705	X61118	0.00482	0.000525	0.001631	0.292879	LMO2
706	AJ004832	0.00482	0.000525	0.001715	0.30393	NTE
707	AB020631	0.001377	0.000525	0.000212	0.379354	PCF11
708	AB002359	0.00482	0.000525	2.36E-05	0.271468	PFAS
709	AB012229	0.001377	0.000525	0.000168	-0.59579	PFKFB3
710	M83088	0.001377	0.000525	3.50E-05	0.439367	PGM1
711	X84908	0.001377	0.000525	2.25E-05	0.331887	PHKB
712	U48250	0.001377	0.000525	8.51E-05	-0.2234	PRKCBP2
713	AB007851	0.000344	0.000525	1.95E-05	0.481768	PRPSAP2
714	X97267	0.00482	0.000525	0.000303	0.211707	PTPRCAP
715	M64595	0.00482	0.000525	0.004436	0.170959	RAC2
716	S59049	0.001377	0.000525	0.000915	-0.61362	RGS1
717	AL050267	0.00482	0.000525	0.000204	0.311003	SAMHD1
718	W28498	0.00482	0.000525	1.70E-05	-0.57386	SAR1
719	W27050	0.00482	0.000525	2.37E-05	-0.587	SFPQ
720	X92762	0.00482	0.000525	0.000116	0.283179	TAZ
721	U18422	0.001377	0.000525	0.000279	-0.14486	TFDP2
722	D87127	0.001377	0.000525	0.000126	-0.32216	TLOC1
723	U12595	0.001377	0.000525	1.07E-05	0.347309	TRAP1
724	AF046024	0.00482	0.000525	0.000469	0.405378	UBE1C
725	AF032456	0.001377	0.000525	5.89E-05	0.269833	UBE2G2
726	Y09723	0.00482	0.000525	0.000854	-0.23772	ZNF151
727	AL031778	0.00482	0.000525	0.000239	0.178561	
728	AL049218	0.00482	0.000525	0.001951	0.238837	
729	AL080216	0.00482	0.000525	0.000349	0.311531	
730	L00352	0.00482	0.000525	0.005084	-0.39882	

731	S79267	0.00482	0.000525	0.000908	-0.19945	
732	U94902	0.00482	0.000525	0.002556	-0.17833	
733	AA206524	0.000344	0.000567	0.000172	0.161868	BART1
734	AA926959	0.000344	0.000567	8.47E-05	0.169915	CKS1
735	M27543	0.000344	0.000567	0.000319	-0.48924	GNAI3
736	AF019386	0.000344	0.000567	0.000399	-0.18103	HS3ST1
737	AB006537	0.000344	0.000567	0.000658	-0.1547	IL1RAP
738	AJ001306	0.000344	0.000567	5.70E-05	0.338818	INADL
739	AB011116	0.000344	0.000567	0.000355	0.25593	KIAA0544
740	AB029014	0.000344	0.000567	0.001352	-0.1261	KIAA1091
741	AB029027	0.000344	0.000567	0.00209	0.180974	KIAA1104
742	M10901	0.000344	0.000567	4.00E-05	-0.42455	NR3C1
743	D30036	0.000344	0.000567	5.62E-05	-0.15539	PITPN
744	U47077	0.000344	0.000567	0.001173	0.30799	PRKDC
745	AF006751	0.000344	0.000567	3.40E-05	-0.23462	RRBP1
746	AB006198	0.000344	0.000567	0.001465	0.256734	SART1
747	D63780	0.000344	0.000567	0.00021	0.374406	STK25
748	W28892	0.000344	0.000567	8.26E-05	0.803602	SUI1
749	M74524	0.000344	0.000567	0.000421	-0.31531	UBE2A
750	AL031230	0.000344	0.000567	6.83E-05	0.272378	
751	AF057160	0.001377	0.000588	0.000279	0.307281	ADPRTL1
752	M74491	0.001377	0.000588	3.02E-05	0.170825	ARF3
753	AL120559	0.001377	0.000588	4.80E-05	-0.64478	ARPP-19
754	D13630	0.001377	0.000588	3.01E-05	-0.42457	BZAP45
755	U83246	0.001377	0.000588	0.003502	0.133045	CPNE1
756	AL050390	0.001377	0.000588	0.000139	0.231898	DKFZP564O043
757	D13315	0.001377	0.000588	0.000203	0.371377	GLO1
758	H12458	0.001377	0.000588	5.42E-05	-0.22578	H12458 yj12d03.s1
759	AI347088	0.001377	0.000588	0.000151	0.321012	HMG17L3
760	X59770	0.001377	0.000588	0.001417	-0.36292	IL1R2
761	AB007855	0.000344	0.000588	1.02E-05	0.086396	KIAA0395
762	AB016816	0.001377	0.000588	0.000751	0.146218	MASL1
763	U07132	0.001377	0.000588	0.002035	-0.27336	NR1H2
764	AB019409	0.001377	0.000588	0.001479	0.154377	PDL-108
765	AB020641	0.001377	0.000588	0.00342	0.174568	PFTK1
766	AL050259	0.001377	0.000588	0.001864	0.272972	RAB2L
767	AA099265	0.001377	0.000588	0.000614	0.38275	RECK
768	X75042	0.001377	0.000588	6.85E-05	-0.39572	REL
769	AL050290	0.001377	0.000588	0.002426	-0.28771	SAT
770	AJ006417	0.001377	0.000588	0.000125	-0.18595	TBCD
771	X02812	0.001377	0.000588	1.78E-05	-0.16423	TGFB1
772	AL050262	0.001377	0.000588	0.0031	0.348226	TLR1
773	X16576	0.001377	0.000588	9.49E-05	0.431692	ZNF46
774	X91249	0.000344	0.000609	1.04E-05	-0.3925	ABCG1
775	Y00486	0.000344	0.000609	0.000297	0.259418	APRT

776	U10473	0.000344	0.000609	0.000103	-0.15424	B4GALT1
777	AB014595	0.000344	0.000609	5.19E-05	0.320955	CUL4B
778	Y15227	0.000344	0.000609	4.08E-05	0.222481	DLEU1
779	U85267	0.000344	0.000609	0.000131	0.142894	DSCR1
780	AB019036	0.000344	0.000609	0.000336	0.177649	GGPS1
781	U90313	0.000344	0.000609	0.001838	-0.25377	GSTTLp28
782	L42243	0.000344	0.000609	0.000201	0.403838	HUMIFNAM08
783	X16983	0.000344	0.000609	0.000317	0.232935	ITGA4
784	AB002368	0.000344	0.000609	0.001709	0.215217	KIAA0370
785	AI521453	0.000344	0.000609	0.000707	-0.22735	PC4
786	Y08110	0.000344	0.000609	9.87E-05	0.260436	SORL1
787	D38122	0.000344	0.000609	6.27E-05	-0.61781	TNFSF6
788	U49278	0.000344	0.000609	0.000173	0.204424	UBE2V1
789	X99050	0.000344	0.000609	7.72E-05	0.289751	UVRAG
790	Z93930	0.000344	0.000609	0.00015	-0.26558	XBP1
791	AF015767	0.000344	0.000659	0.000199	0.578977	BRE
792	M34677	0.000344	0.000659	0.000647	0.198622	F8A
793	J00210	0.000344	0.000659	0.002453	-0.18828	IFNA1
794	AJ007583	0.000344	0.000659	0.00506	-0.12644	LARGE
795	M36881	0.000344	0.000659	0.000302	0.328248	LCK
796	X70326	0.000344	0.000659	0.000132	-0.58974	MACMARCKS
797	M64571	0.000344	0.000659	0.000158	0.157573	MAP4
798	AI345944	0.000344	0.000659	0.000363	0.311507	NDUFB1
799	D23662	0.000344	0.000659	0.000171	0.289452	NEDD8
800	M14630	0.000344	0.000659	1.26E-05	-0.1626	PTMA
801	D64015	0.000344	0.000659	0.001012	0.195679	TIAL1
802	M63582	0.000344	0.000659	2.66E-05	-0.39175	
803	U79300	0.000344	0.000659	0.000196	-0.16218	
804	D29805	0.00482	0.000812	0.000289	-0.23044	B4GALT1
805	U47414	0.001377	0.000812	0.000137	0.262974	CCNG2
806	L33930	0.001377	0.000812	5.56E-06	0.343203	CD24
807	AL050164	0.00482	0.000812	0.000345	0.307729	CDYL
808	D10040	0.001377	0.000812	1.49E-05	-0.45708	FACL2
809	M36820	0.00482	0.000812	7.67E-05	-0.49075	GRO2
810	U77948	0.00482	0.000812	0.000511	0.286776	GTF2I
811	X56681	0.00482	0.000812	0.000503	-0.18359	JUND
812	AF070569	0.00482	0.000812	0.000446	-0.6104	MGC14376
813	W28205	0.00482	0.000812	0.00017	-0.21741	MKLN1
814	U61981	0.001377	0.000812	0.000725	0.203996	MSH3
815	AB014547	0.001377	0.000812	7.73E-05	0.217806	MTMR4
816	AL050366	0.00482	0.000812	0.001126	0.421541	OGT
817	U89606	0.001377	0.000812	6.13E-05	-0.19512	PDXK
818	D10495	0.00482	0.000812	0.000433	0.290156	PRKCD
819	D42063	0.001377	0.000812	0.000346	-0.52828	RANBP2
820	H68340	0.00482	0.000812	0.004081	-0.3419	RNAHP
821	AF059617	0.001377	0.000812	0.00012	-0.27807	SNK

822	AB028950	0.00482	0.000812	0.000365	0.313606	TLN1
823	L41690	0.001377	0.000812	0.000109	0.401776	TRADD
824	X95384	0.00482	0.000812	0.00053	0.327055	UK114
825	X98054	0.00482	0.001094	4.71E-05	-0.12615	CREBL1
826	J05036	0.00482	0.001094	0.00171	0.064463	CTSE
827	AF001434	0.00482	0.001094	0.000161	-0.26223	EHD1
828	L18960	0.00482	0.001094	3.26E-05	-0.38369	EIF1A
829	AB014555	0.00482	0.001094	0.001608	-0.18202	KIAA0655
830	X76057	0.00482	0.001094	0.000352	0.193745	MPI
831	X74594	0.00482	0.001094	0.000352	0.439326	RBL2
832	AF044309	0.00482	0.001094	0.000217	-0.2163	STX11
833	U07158	0.00482	0.001094	0.000122	-0.2301	STX4A
834	L40386	0.00482	0.001094	7.97E-05	-0.19863	TFDP2
835	H97470	0.00482	0.001094	0.000624	-0.10587	
836	U78027	0.00482	0.001094	0.000804	0.340784	
837	U50534	0.001377	0.001345	0.00039	0.250627	13CDNA73
838	X55330	0.001377	0.001345	9.30E-05	0.493025	AGA
839	L19605	0.001377	0.001345	0.004442	0.183134	ANXA11
840	Y00097	0.001377	0.001345	4.42E-05	0.409932	ANXA6
841	U26455	0.00482	0.001345	0.000705	0.499049	ATM
842	AF047473	0.001377	0.001345	5.14E-05	0.226	BUB3
843	M95724	0.00482	0.001345	0.002166	-0.46553	CENPC1
844	AB014558	0.001377	0.001345	0.004662	-0.44793	CRY2
845	R38263	0.001377	0.001345	0.00048	-0.12843	DJ347H13.4
846	AI434146	0.001377	0.001345	0.000397	0.187485	DKFZp570I0164
847	D12686	0.00482	0.001345	0.008744	-0.11456	EIF4G1
848	AF059611	0.00482	0.001345	0.000694	-0.27343	ENC1
849	X59834	0.001377	0.001345	0.004986	-0.34836	GLUL
850	D64142	0.001377	0.001345	0.000169	0.293999	H1FX
851	U51333	0.001377	0.001345	0.000376	0.273402	HK3
852	M59488	0.001377	0.001345	0.001357	-0.13313	HUMS100B3
853	X58529	0.001377	0.001345	0.000417	1.04789	IGHM
854	D79983	0.001377	0.001345	2.97E-05	0.387491	KIAA0161
855	AB002370	0.00482	0.001345	0.00052	0.425557	KIAA0372
856	AB007863	0.001377	0.001345	0.000128	0.29668	KIAA0403
857	AB014549	0.001377	0.001345	0.001505	0.42387	KIAA0649
858	AB020711	0.00482	0.001345	0.002079	0.222346	KIAA0904
859	AB002357	0.001377	0.001345	0.001045	0.317849	KIF3B
860	U09284	0.00482	0.001345	0.000792	-0.23635	LIMS1
861	D50810	0.001377	0.001345	5.17E-05	-0.1859	LNPEP
862	U18259	0.001377	0.001345	0.000153	0.229322	MHC2TA
863	AF041080	0.00482	0.001345	0.001964	0.367098	MN7
864	X70991	0.001377	0.001345	0.00203	-0.14032	NAB2
865	AC002045	0.00482	0.001345	0.00028	0.326033	NPIP
866	U92538	0.001377	0.001345	0.00149	0.2372	ORC5L
867	U24153	0.001377	0.001345	0.00018	-0.36291	PAK2

868	Z49194	0.001377	0.001345	0.000519	0.215733	POU2AF1
869	AF016371	0.001377	0.001345	0.001059	0.240562	PPIH
870	AF020736	0.001377	0.001345	6.26E-05	-0.32893	PSMC4
871	D11327	0.001377	0.001345	0.00019	-0.74969	PTPN7
872	AF098799	0.00482	0.001345	0.001893	-0.3646	RANBP7
873	M22995	0.001377	0.001345	0.005586	0.270032	RAP1A
874	L11566	0.001377	0.001345	0.000291	0.17032	RPL18
875	U71364	0.001377	0.001345	0.000276	-0.24064	SERPINB9
876	X07834	0.00482	0.001345	0.000362	-0.21917	SOD2
877	X05839	0.001377	0.001345	0.000779	-0.20819	TGFB1
878	AB000509	0.001377	0.001345	3.63E-05	0.460686	TRAF5
879	U82130	0.001377	0.001345	4.69E-05	-0.36064	TSG101
880	L16842	0.001377	0.001345	0.001533	0.189597	UQCRC1
881	X51521	0.001377	0.001345	0.000379	-0.62845	VIL2
882	M86400	0.001377	0.001345	0.000132	-0.30595	YWHAZ
883	AF041259	0.001377	0.001345	0.001393	0.202001	ZNF217
884	AA977136	0.001377	0.001345	0.001953	0.095364	
885	AI624038	0.001377	0.001345	0.001833	-0.16137	
886	AL050148	0.00482	0.001345	0.000905	0.266795	
887	HG2709-HT2805	0.001377	0.001345	0.000134	-0.22645	
888	HG3227-HT3404	0.001377	0.001345	4.02E-05	-0.23244	
889	M28225	0.00482	0.001345	0.001444	-0.95152	
890	U80017	0.001377	0.001345	0.004917	0.171432	
891	X55544	0.001377	0.001467	0.001049	-0.12406	ATF1
892	X52560	0.001377	0.001467	8.17E-05	-0.50375	CEBPB
893	AA044787	0.001377	0.001467	0.001147	0.289086	CNOT8
894	AF017790	0.001377	0.001467	6.88E-06	0.382661	HEC
895	D00749	0.001377	0.001467	0.000131	-0.10539	HUMCD7G3
896	AB007890	0.001377	0.001467	0.000838	0.200677	KIAA0430
897	L35251	0.001377	0.001467	0.000873	0.12909	MFAP3
898	AF098638	0.001377	0.001467	0.000684	-0.18761	RAB5EP
899	AB004857	0.001377	0.001467	0.000471	0.23048	SLC11A2
900	U53347	0.001377	0.001467	0.001367	-0.13658	SLC1A5
901	U04847	0.001377	0.001467	0.000403	0.117176	SMARCB1
902	M92843	0.001377	0.001467	3.30E-05	-1.37866	ZFP36
903	AF033199	0.001377	0.001467	0.00019	0.237743	ZNF204
904	AC004893	0.001377	0.001467	0.000617	-0.25759	
905	AL050151	0.001377	0.001467	8.03E-06	-0.80887	
906	U80770	0.001377	0.001467	0.006738	-0.12644	
907	W27675	0.00482	0.001614	0.005157	0.468709	CDA02
908	AI056696	0.00482	0.001614	0.000665	0.215941	CETN3
909	AF062536	0.00482	0.001614	0.005001	0.197482	CUL1
910	D29643	0.00482	0.001614	0.0005	0.157183	DDOST
911	AA181196	0.00482	0.001614	0.000166	0.119162	FLJ11712
912	W07033	0.001377	0.001614	0.000136	0.347648	GMFG
913	Z18859	0.00482	0.001614	0.000684	0.181514	GNAT2

914	U83660	0.00482	0.001614	0.00114	0.136411	HSU83660
915	AA628946	0.00482	0.001614	0.002684	0.337197	KHSRP
916	D13626	0.00482	0.001614	0.005837	0.254138	KIAA0001
917	AB002340	0.00482	0.001614	0.002977	0.168464	KIAA0342
918	AB002353	0.001377	0.001614	0.000119	0.305921	KIAA0355
919	U32849	0.00482	0.001614	0.000272	0.345048	NMI
920	S79219	0.00482	0.001614	0.000119	0.167463	PCCA
921	L37127	0.00482	0.001614	0.010173	0.103446	POLR2J
922	M35416	0.00482	0.001614	0.001433	0.33505	RALB
923	X76061	0.00482	0.001614	0.000273	0.378113	RBL2
924	AF061741	0.00482	0.001614	0.004586	0.221278	SDR1
925	D31891	0.001377	0.001614	0.000819	0.161458	SETDB1
926	W26406	0.00482	0.001614	0.000479	0.300512	SIAH1
927	X84002	0.00482	0.001614	0.000699	0.143479	TAF2J
928	U81006	0.00482	0.001614	0.003151	0.255479	TM9SF2
929	U69108	0.00482	0.001614	0.000657	0.208286	TRAF5
930	S66666	0.00482	0.001614	0.002417	0.119478	
931	U84388	0.00482	0.001719	0.000197	-0.18606	CRADD
932	L08069	0.00482	0.001719	0.001985	-0.31866	DNAJA1
933	U41514	0.00482	0.001719	9.38E-05	-0.44803	GALNT1
934	M69013	0.001377	0.001719	6.26E-05	-0.1948	GNA11
935	L11706	0.00482	0.001719	0.001422	-0.16675	LIPE
936	R92331	0.00482	0.001719	0.000198	-0.24196	MT1E
937	X64318	0.00482	0.001719	0.006253	-0.37391	NFIL3
938	X12458	0.00482	0.001719	0.001489	-0.33668	P3
939	M25393	0.00482	0.001719	0.000958	-0.23304	PTPN2
940	M59465	0.00482	0.001719	0.0002	-0.96074	TNFAIP3
941	AF084260	0.00482	0.001719	0.001063	-0.39491	TRIP15
942	HG2149-HT2219	0.00482	0.001719	0.001437	-0.14432	
943	AB021663	0.00482	0.001963	0.00027	-0.13923	ATF5
944	AL080209	0.00482	0.001963	0.000337	0.437957	DKFZP586F2423
945	M34641	0.00482	0.001963	0.002352	-0.14552	FGFR1
946	AL096714	0.001377	0.001963	0.000469	0.224782	FLJ20113
947	AB011124	0.001377	0.001963	0.000101	-0.17709	KIAA0552
948	AB020633	0.001377	0.001963	0.00082	0.308616	KIAA0826
949	AB029020	0.001377	0.001963	0.00061	0.3824	KIAA1097
950	X76220	0.001377	0.001963	7.21E-05	0.444366	MAL
951	AF040964	0.00482	0.001963	0.001161	-0.54746	MGC4701
952	U91512	0.001377	0.001963	0.00035	-0.55826	NINJ1
953	U60325	0.00482	0.001963	0.000288	-0.14386	POLG
954	Z15108	0.001377	0.001963	0.000107	0.176424	PRKCZ
955	Y08262	0.001377	0.001963	0.000183	0.377974	SCA2
956	U30246	0.001377	0.001963	0.000209	-0.25952	SLC12A2
957	J04137	0.001377	0.001963	0.000641	-0.22175	SSA2
958	M38449	0.001377	0.001963	0.0004	-0.29059	TGFB1
959	AC005757	0.00482	0.001963	0.000169	0.387439	

960	HG825-HT825	0.001377	0.001963	0.000553	-0.19964	
961	AF047348	0.001377	0.002207	0.000292	0.202669	APBA2
962	AF053977	0.001377	0.002207	0.003143	0.134266	CDC23
963	AF083322	0.001377	0.002207	0.000344	0.272282	CEP1
964	AL050369	0.001377	0.002207	0.001224	0.241992	DKFZP566J153
965	D32257	0.001377	0.002207	0.000238	0.300058	GTF3A
966	M65217	0.001377	0.002207	0.000232	0.249614	HSF2
967	AB014574	0.001377	0.002207	0.000606	0.130056	KIAA0674
968	AB029023	0.001377	0.002207	0.000219	0.219428	KIAA1100
969	Z34975	0.001377	0.002207	8.88E-05	0.41432	LDLC
970	D83597	0.001377	0.002207	0.000136	0.249838	LY64
971	U09759	0.001377	0.002207	0.000842	0.330751	MAPK9
972	U59302	0.001377	0.002207	0.000241	0.309348	NCOA1
973	AJ005698	0.001377	0.002207	0.004173	0.139618	PARN
974	X54871	0.001377	0.002207	0.010035	0.119258	RAB5B
975	AL080198	0.001377	0.002207	0.002866	0.251598	RENT2
976	M74447	0.001377	0.002207	0.000444	0.093537	TAP2
977	J04973	0.001377	0.002207	0.011696	0.141705	UQCRC2
978	U90902	0.001377	0.002207	0.001336	0.246217	
979	U94333	0.001377	0.002323	0.004818	-0.13898	C1QR
980	U60808	0.001377	0.002323	0.000374	-0.12217	CDS1
981	L08069	0.001377	0.002323	0.002161	-0.29982	DNAJA1
982	AA552140	0.001377	0.002323	0.003368	-0.22604	E2F4
983	M31210	0.001377	0.002323	0.000124	-0.33555	EDG1
984	AI189287	0.001377	0.002323	0.002445	-0.24115	H1F2
985	W25934	0.001377	0.002323	0.003385	-0.32382	JTV1
986	Z98046	0.001377	0.002323	0.000122	-0.33551	MAGED2
987	L76571	0.001377	0.002323	0.009985	-0.12617	NR0B2
988	AF071504	0.001377	0.002323	0.000191	-0.14267	STX11
989	X56687	0.001377	0.002323	0.00011	-0.29728	UBTF
990	AI097085	0.001377	0.002323	0.000941	-0.16209	
991	AA114830	0.001377	0.002503	0.000293	0.272601	AKAP10
992	AI991631	0.001377	0.002503	0.000132	-0.11786	BRD4
993	U04343	0.001377	0.002503	4.45E-05	-0.25478	CD86
994	M12824	0.001377	0.002503	0.008271	-0.34597	CD8A
995	U89896	0.001377	0.002503	0.006997	-0.2182	CSNK1G2
996	AI432401	0.001377	0.002503	0.006072	0.32631	FGL2
997	AA176780	0.001377	0.002503	0.001296	0.14235	HSA249128
998	M21188	0.001377	0.002503	0.000165	0.251899	IDE
999	U43572	0.001377	0.002503	0.000128	0.318327	NAGLU
1000	X02751	0.001377	0.002503	0.000359	-0.2229	NRAS
1001	AF069250	0.001377	0.002503	0.00135	0.476217	OA48-18
1002	D25328	0.001377	0.002503	0.000171	0.125335	PFKP
1003	AF010312	0.001377	0.002503	0.001216	-0.47628	PIG7
1004	M34668	0.001377	0.002503	0.000421	0.181315	PTPRA
1005	AF061836	0.001377	0.002503	0.001026	0.21847	RASSF1

1006	AI535653	0.001377	0.002503	0.001712	0.34571	SC4MOL
1007	X75755	0.001377	0.002503	0.003813	-0.2236	SFRS2
1008	W16505	0.001377	0.002503	0.001699	0.101763	SNRPD2
1009	L31529	0.001377	0.002503	0.000325	0.144265	SNTB1
1010	D86970	0.001377	0.002503	0.000219	0.218777	TIAF1
1011	AL050223	0.001377	0.002503	0.002632	0.2458	VAMP2
1012	AA877215	0.001377	0.002503	0.008439	-0.17878	
1013	AL049435	0.001377	0.002503	0.000111	0.194323	
1014	M76180	0.001377	0.002575	0.000698	0.162775	DDC
1015	M94065	0.001377	0.002575	0.000426	0.156894	DHODH
1016	J04988	0.001377	0.002575	6.17E-05	-0.22304	HSPCB
1017	Z68907	0.001377	0.002575	0.000305	0.391111	IDH3G
1018	J03909	0.001377	0.002575	0.000837	-0.35709	IFI30
1019	AB011104	0.001377	0.002575	0.000729	0.227798	KIAA0532
1020	AB011173	0.001377	0.002575	0.000585	0.283714	KIAA0601
1021	U70322	0.001377	0.002575	0.000177	-0.41259	KPNB2
1022	D86961	0.001377	0.002575	0.001925	-0.19403	LHFPL2
1023	AF052111	0.001377	0.002575	0.000738	0.249468	LOC51172
1024	AJ224875	0.001377	0.002575	0.005091	0.139606	MGC2840
1025	M21985	0.001377	0.002575	0.001409	-0.102	NR2C1
1026	J05448	0.001377	0.002575	0.004982	-0.15329	POLR2C
1027	AB006572	0.001377	0.002575	0.000169	0.213636	RMP
1028	AJ011712	0.001377	0.002575	0.011372	0.066711	TNNT1
1029	AJ006973	0.001377	0.002575	0.000101	-0.31773	TOM1
1030	U67122	0.001377	0.002575	0.000364	-0.14274	UBL1
1031	U71598	0.001377	0.002575	0.003508	0.128607	ZNF274
1032	M81118	0.001377	0.002575	0.00023	0.333526	
1033	U61166	0.001377	0.002575	0.003055	-0.14488	
1034	U94902	0.001377	0.002575	0.000137	-0.23298	
1035	Z82244	0.001377	0.002575	0.000258	-0.53938	
1036	M36341	0.001377	0.002788	0.00056	-0.38498	ARF4
1037	L09159	0.001377	0.002788	0.00112	0.474985	ARHA
1038	U68485	0.00482	0.002788	0.006797	0.224774	BIN1
1039	Z22555	0.001377	0.002788	0.005455	-0.16351	CD36L1
1040	D44497	0.00482	0.002788	0.004453	0.131654	CORO1A
1041	L37042	0.00482	0.002788	0.000582	-0.33273	CSNK1A1
1042	M74099	0.001377	0.002788	0.00014	0.389638	CUTL1
1043	AL080159	0.001377	0.002788	0.002335	-0.11101	DKFZP434M154
1044	AF004292	0.001377	0.002788	0.001306	-0.2375	DKFZP566C134
1045	AF088982	0.001377	0.002788	0.001264	-0.22098	DNAJB5
1046	U73704	0.001377	0.002788	0.001412	-0.17508	FAP48
1047	M77810	0.00482	0.002788	0.000209	-0.15854	GATA2
1048	U67369	0.00482	0.002788	0.00347	0.137095	GFI1
1049	D00632	0.001377	0.002788	0.001138	-0.15517	GPX3
1050	X99270	0.001377	0.002788	0.00065	0.191612	HSXQ28ORF
1051	D42041	0.00482	0.002788	0.003705	0.195279	KIAA0088

1052	AA524058	0.001377	0.002788	0.000288	0.360599	LOC51020
1053	U77604	0.001377	0.002788	0.00233	0.296247	MGST2
1054	J04031	0.00482	0.002788	0.000148	0.290038	MTHFD1
1055	AF025794	0.001377	0.002788	0.006763	0.107466	MTRR
1056	D86326	0.001377	0.002788	0.008217	0.124987	P115
1057	U14417	0.001377	0.002788	0.000521	-0.13999	RALGDS
1058	U85611	0.001377	0.002788	0.000126	-0.3879	SIP2-28
1059	U66617	0.001377	0.002788	0.001462	-0.14653	SMARCD1
1060	X59960	0.001377	0.002788	0.005127	-0.11069	SMPD1
1061	AF031166	0.001377	0.002788	0.001219	0.110457	SRP46
1062	U86136	0.001377	0.002788	0.000542	0.149235	TEP1
1063	U16296	0.001377	0.002788	0.00138	0.136848	TIAM1
1064	D50917	0.001377	0.002788	0.000467	0.402091	TRIP-Br2
1065	AC004770	0.001377	0.002788	0.001042	-0.10615	
1066	J03071	0.001377	0.002788	0.0116	0.17732	
1067	D67031	0.00482	0.004163	0.000204	0.543743	ADD3
1068	U68030	0.00482	0.004163	0.000279	-0.16075	CCR6
1069	U41387	0.00482	0.004163	8.67E-05	-0.29576	DDX21
1070	AF084535	0.00482	0.004163	0.002306	0.159095	EPM2A
1071	AI417075	0.00482	0.004163	0.000538	0.330385	FLJ14040
1072	D82348	0.00482	0.004349	0.006063	0.245422	ATIC
1073	AA648295	0.00482	0.004349	0.002422	0.337484	CBX3
1074	U79270	0.00482	0.004349	0.001345	0.460807	COX11
1075	AF071748	0.00482	0.004349	0.002471	0.170315	CTSF
1076	AL080088	0.00482	0.004349	0.000207	0.165357	DKFZP564K2062
1077	AI540318	0.00482	0.004349	0.00055	-0.13789	DNAJB6
1078	U03272	0.00482	0.004349	0.003893	0.101031	FBN2
1079	Z97989	0.00482	0.004349	0.001126	-0.41969	FYN
1080	AF042379	0.00482	0.004349	0.008308	0.176604	GCP2
1081	U73737	0.00482	0.004349	0.00262	-0.14396	HUMMSH06
1082	AF031167	0.00482	0.004349	0.000117	0.201914	IL15
1083	D83778	0.00482	0.004349	0.000504	-0.2149	KIAA0194
1084	AB028965	0.00482	0.004349	0.007277	0.125446	KIAA1042
1085	M79321	0.00482	0.004349	0.003247	-0.21992	LYN
1086	L11284	0.00482	0.004349	0.003994	-0.09508	MAP2K1
1087	AJ000882	0.00482	0.004349	0.00042	0.180413	NCOA1
1088	L41067	0.00482	0.004349	0.000388	0.370635	NFATC3
1089	AF057297	0.00482	0.004349	0.001191	0.521103	OAZ2
1090	X66360	0.00482	0.004349	0.001123	-0.17473	PCTK2
1091	U24183	0.00482	0.004349	0.001156	0.141168	PFKM
1092	L42373	0.00482	0.004349	0.006706	0.165885	PPP2R5A
1093	AB018288	0.00482	0.004349	0.003777	0.184227	RANBP16
1094	M58459	0.00482	0.004349	0.008923	-1.04752	RPS4Y
1095	M60725	0.00482	0.004349	0.001349	-0.10092	RPS6KB1
1096	Y10931	0.00482	0.004349	0.001246	0.194156	SPK

1097	AB004904	0.00482	0.004349	0.000233	-0.31373	SSI-3
1098	AF060798	0.00482	0.004349	0.000809	0.142845	STK16
1099	U66867	0.00482	0.004349	0.011318	0.150812	UBE2I
1100	AB028980	0.00482	0.004349	0.001471	0.265042	USP24
1101	AF052107	0.00482	0.004349	0.002884	0.197902	
1102	AL031985	0.00482	0.004349	0.000181	-0.24089	
1103	D26121	0.00482	0.004349	0.00387	-0.16268	
1104	W28667	0.00482	0.004349	0.004391	0.476395	
1105	AL050157	0.00482	0.004467	0.000289	0.269949	DKFZP586O0120
1106	U31930	0.00482	0.004467	0.000244	0.349997	DUT
1107	AI951946	0.00482	0.004467	8.71E-05	0.401112	HBOA
1108	AB002354	0.00482	0.004467	0.001517	-0.13368	KIAA0356
1109	M36067	0.00482	0.004467	8.15E-05	0.277858	LIG1
1110	J02783	0.00482	0.004467	0.002151	-0.21979	P4HB
1111	M37238	0.00482	0.004467	0.005333	-0.15474	PLCG2
1112	M99438	0.00482	0.004467	6.20E-05	-0.36844	TLE3
1113	Z97630	0.00482	0.004467	0.002794	0.217849	
1114	D14874	0.00482	0.005608	0.000611	-0.55358	ADM
1115	L08177	0.00482	0.005608	0.000434	-0.49252	EBI2
1116	U09510	0.00482	0.005608	5.27E-05	-0.57567	GARS
1117	L05424	0.00482	0.005608	0.000114	-0.39048	HUMSCG19
1118	X13956	0.00482	0.005608	0.004098	0.187622	MGC10471
1119	U88620	0.00482	0.005608	0.00074	0.345628	OGG1
1120	M29551	0.00482	0.005608	0.000471	0.319301	PPP3CB
1121	AF068836	0.00482	0.005608	0.000323	-0.23628	PSCDBP
1122	U08316	0.00482	0.005608	0.0006	0.205899	RPS6KA3
1123	J02966	0.00482	0.005608	0.000498	-0.11291	SLC25A4
1124	AF107463	0.00482	0.005608	0.002824	-0.36924	SPF30
1125	AB000450	0.00482	0.005608	0.000256	-0.24717	VRK2
1126	AF070590	0.00482	0.005608	0.000834	0.127523	
1127	AF001383	0.00482	0.006065	0.002075	0.16512	BIN1
1128	AF026291	0.00482	0.006065	0.000385	-0.16859	CCT4
1129	D63877	0.00482	0.006065	0.005226	-0.13956	KIAA0157
1130	U14383	0.00482	0.006065	0.002623	-0.18669	MUC8
1131	U68140	0.00482	0.006065	0.000677	0.172443	NVL
1132	L25441	0.00482	0.006065	0.000613	-0.17207	PGGT1B
1133	U46751	0.00482	0.006065	0.000578	-0.38675	SQSTM1
1134	HG4740-HT5187	0.00482	0.006065	0.00867	0.146562	
1135	W26851	0.00482	0.006065	0.002052	0.312992	
1136	U78735	0.00482	0.006347	0.000529	-0.09197	ABCA3
1137	Y12226	0.00482	0.006347	0.000397	-0.21303	AP1G1
1138	D38293	0.00482	0.006347	0.002894	-0.24373	AP3M2
1139	X14046	0.00482	0.006347	0.001084	0.134786	CD37
1140	AF026004	0.00482	0.006347	0.008622	-0.07494	CLCN2
1141	U46023	0.00482	0.006347	0.000273	-0.17969	CXorf6

1142	AL080178	0.00482	0.006347	0.000683	0.260343	DKFZP434K171
1143	AL080118	0.00482	0.006347	0.001904	-0.28696	DKFZP564F1123
1144	AL050197	0.00482	0.006347	0.004294	0.233045	DKFZP586D0623
1145	X68277	0.00482	0.006347	0.011411	-0.42385	DUSP1
1146	X03674	0.00482	0.006347	0.008478	0.174463	G6PD
1147	Y13286	0.00482	0.006347	0.004068	0.134985	GDI2
1148	U19247	0.00482	0.006347	0.000589	-0.29688	HSINFGRA7
1149	AB023163	0.00482	0.006347	0.002537	0.194491	HYPH
1150	L36818	0.00482	0.006347	0.007182	0.204818	INPPL1
1151	U51127	0.00482	0.006347	0.003952	0.108702	IRF5
1152	M15395	0.00482	0.006347	0.001863	0.402323	ITGB2
1153	U51336	0.00482	0.006347	0.008615	0.336527	ITPK1
1154	AJ000008	0.00482	0.006347	0.000256	-0.14181	PIK3C2G
1155	AI126004	0.00482	0.006347	0.000954	0.262925	SAS10
1156	AF051325	0.00482	0.006347	0.000144	-0.43952	SH2D2A
1157	U79528	0.00482	0.006347	0.002518	0.158101	SR-BP1
1158	U52426	0.00482	0.006347	9.31E-05	0.411984	STIM1
1159	AB018339	0.00482	0.006347	0.000751	0.199758	SYNE-1B
1160	D43642	0.00482	0.006347	0.0005	0.305805	TCFL1
1161	D29767	0.00482	0.006347	0.003934	-0.09702	TEC
1162	M92383	0.00482	0.006347	0.001466	0.219769	TMSB10
1163	AA192359	0.00482	0.006347	0.00028	0.17619	TRN-SR
1164	AC004472	0.00482	0.006347	0.002169	-0.15115	
1165	AF052138	0.00482	0.006347	0.000189	0.441167	
1166	X15674	0.00482	0.006347	0.007899	-0.10738	
1167	Z82215	0.00482	0.006347	0.002527	0.153792	
1168	AF070523	0.00482	0.006634	0.00037	0.437983	JWA
1169	D13641	0.00482	0.006634	0.000776	0.275308	KIAA0016
1170	X79204	0.00482	0.006634	0.000182	0.256049	SCA1
1171	AB015718	0.00482	0.006634	0.001172	0.202412	STK10
1172	AF059575	0.00482	0.006634	0.000563	-0.18074	
1173	M74089	0.00482	0.006634	0.00076	0.187888	
1174	U44111	0.00482	0.006634	0.003845	0.105361	
1175	AJ243310	0.00482	0.006921	0.000945	-0.97643	C14orf3
1176	W26854	0.00482	0.006921	0.011098	-0.13774	DKFZP434D156
1177	U88629	0.00482	0.006921	0.001778	-0.16763	ELL2
1178	M59830	0.00482	0.006921	0.000221	-1.12882	HSPA1B
1179	M95929	0.00482	0.006921	0.004606	-0.34536	PMX1
1180	M57399	0.00482	0.006921	0.010231	-0.14331	PTN
1181	N25117	0.00482	0.006921	0.002068	-0.16335	RPS26
1182	AL049940	0.00482	0.006921	0.001149	-0.42489	RYBP
1183	U39318	0.00482	0.006921	0.001097	-0.24533	UBE2D3
1184	Z29331	0.00482	0.006921	0.000193	-0.15851	UBE2H
1185	M55682	0.00482	0.006921	0.010264	-0.10921	
1186	S58544	0.00482	0.006921	0.005501	-0.11193	

1187	L13687	0.00482	0.007311	0.002185	0.114008	ARL2
1188	M88714	0.00482	0.007311	0.002075	0.114833	BDKRB2
1189	AL050173	0.00482	0.007311	0.001866	0.128954	C21orf25
1190	M33680	0.00482	0.007311	0.002612	0.134487	CD81
1191	X05299	0.00482	0.007311	0.003837	0.171613	CENPB
1192	X16832	0.00482	0.007311	0.000578	0.177395	CTSH
1193	U83410	0.00482	0.007311	0.005207	0.219569	CUL2
1194	AL050018	0.00482	0.007311	0.003938	0.220539	DKFZP564B116
1195	AL080063	0.00482	0.007311	0.006562	0.186332	DKFZP564I052
1196	AL050286	0.00482	0.007311	0.000767	0.221397	DKFZP586A011
1197	X63692	0.00482	0.007311	0.003174	0.172997	DNMT1
1198	AA522537	0.00482	0.007311	0.002762	0.113812	ELAC2
1199	AI183417	0.00482	0.007311	0.006167	0.101739	GABPB1
1200	X62534	0.00482	0.007311	0.000973	0.195089	HMG2
1201	D50532	0.00482	0.007311	0.001268	0.159735	HML2
1202	AJ006591	0.00482	0.007311	0.001379	0.1682	HSA6591
1203	Y00796	0.00482	0.007311	0.000438	0.386166	ITGAL
1204	AB018301	0.00482	0.007311	0.008701	0.138344	KIAA0758
1205	AB020694	0.00482	0.007311	0.002526	0.205561	KIAA0887
1206	AB023198	0.00482	0.007311	0.000409	0.275051	KIAA0981
1207	AB028958	0.00482	0.007311	0.001533	0.117614	KIAA1035
1208	U66711	0.00482	0.007311	0.006567	0.260368	LY6E
1209	L13744	0.00482	0.007311	0.007658	0.19599	MLLT3
1210	Y09631	0.00482	0.007311	0.000769	0.309898	PIBF1
1211	L77213	0.00482	0.007311	0.001122	0.247214	PMVK
1212	X73478	0.00482	0.007311	0.000681	0.242238	PPP2R4
1213	U94319	0.00482	0.007311	0.000688	0.337656	PSIP2
1214	U27516	0.00482	0.007311	0.000222	0.194938	RAD52
1215	W25793	0.00482	0.007311	0.000438	0.258505	RNF3
1216	X06617	0.00482	0.007311	0.002581	0.116631	RPS11
1217	Z25749	0.00482	0.007311	0.001419	0.123333	RPS7
1218	U80760	0.00482	0.007311	0.007371	0.161214	TNRC1
1219	L27071	0.00482	0.007311	0.000638	0.372837	TXK
1220	AL031427	0.00482	0.007311	0.000541	0.367004	
1221	AL109722	0.00482	0.007311	0.00187	0.134304	
1222	X15675	0.00482	0.007311	0.011165	0.131908	
1223	AL050089	0.00482	0.007852	0.001906	-0.23061	BAZ1A
1224	L22005	0.00482	0.007852	0.002439	-0.22532	CDC34
1225	AB014679	0.00482	0.007852	0.003059	-0.13664	CHST2
1226	X77956	0.00482	0.007852	0.000689	-0.22743	ID1
1227	AI814466	0.00482	0.007852	0.001127	-0.1955	VAMP5
1228	HG4074-HT4344	0.00482	0.007852	0.000964	-0.17461	
1229	AF005050	0.00482	0.008059	0.001761	0.230395	DNPEP
1230	J03909	0.00482	0.008059	0.000125	-0.18353	IFI30
1231	X59841	0.00482	0.008059	0.000226	0.265756	PBX3
1232	AI819942	0.00482	0.009314	0.002286	0.326115	02-Sep

1233	D86981	0.00482	0.009314	0.003441	0.319525	APPBP2
1234	Y10805	0.00482	0.009314	0.002583	0.183496	HRMT1L2
1235	U51127	0.00482	0.009314	0.00212	0.282678	IRF5
1236	U14970	0.00482	0.009314	0.000561	0.144991	RPS5
1237	AI813532	0.00482	0.009314	0.00037	-0.41933	TNFRSF1B
1238	Y15228	0.00482	0.010363	0.002026	-0.17032	DLEU2
1239	AA926957	0.00482	0.010363	0.000909	-0.22483	FLJ10534
1240	AA554945	0.00482	0.010363	0.001827	-0.14301	FLJ10803
1241	AJ001383	0.00482	0.010363	0.001968	-0.3226	LY94
1242	M97676	0.00482	0.010363	0.010011	-0.16313	MSX1
1243	AF002020	0.00482	0.010363	0.001278	-0.1736	NPC1
1244	U25975	0.00482	0.010363	0.000764	-0.24651	PAK2
1245	X66363	0.00482	0.010363	0.000837	-0.4179	PCTK1
1246	D87957	0.00482	0.010363	0.004418	-0.14751	RQCD1
1247	AI610467	0.00482	0.010363	0.000699	-0.17683	SMG1
1248	AJ012008	0.00482	0.010363	0.002571	-0.32997	
1249	AJ012008	0.00482	0.010363	0.001638	-0.16204	

Table II: Gene Expression Profile from PBMCs of MS vs. Healthy- Highest Scoring Genes (Bonfferoni analysis)

SEQ ID NO:	Identifier	TNOM PValue	Info PValue	t-Test PValue	Log FoldChange	Symbol
1250	AA203527	1.37E-05	1.61E-06	1.18E-07	0.281992	RPP20
1251	AA780049	7.44E-05	2.35E-05	7.39E-07	0.54912	FLJ21439
1252	AA845349	7.44E-05	0.0001187	7.78E-07	0.457176	TRIP7
1253	AA902713	2.11E-06	1.99E-06	1.44E-06	0.474378	
1254	AB002344	7.44E-05	5.92E-05	8.48E-07	-1.00068	KIAA0346
1255	AB002347	2.11E-06	1.33E-07	7.19E-10	0.371731	KIAA0349
1256	AB002348	1.37E-05	3.86E-06	2.49E-07	0.576346	KIAA0350
1257	AB002386	2.11E-06	7.73E-07	5.34E-09	0.586117	EZH1
1258	AB002448	1.37E-05	5.01E-06	2.45E-07	0.468926	
1259	AB007891	1.37E-05	3.86E-06	3.99E-05	0.196376	KIAA0431
1260	AB007895	1.37E-05	5.01E-06	9.61E-07	0.186643	KIAA0435
1261	AB007927	2.11E-06	1.99E-06	2.12E-07	0.323787	RERE
1262	AB007960	2.11E-06	9.54E-07	7.96E-06	0.447772	SH3GLB1
1263	AB008775	0.0003443	0.0003041	1.88E-06	-0.80745	AQP9
1264	AB011004	0.0003443	7.05E-06	1.41E-06	-1.34073	UAP1
1265	AB011108	1.37E-05	5.05E-07	4.39E-07	0.453498	PRP4
1266	AB011113	1.37E-05	7.05E-06	3.74E-07	0.444795	WDR7
1267	AB011115	1.37E-05	5.05E-07	3.39E-07	0.382809	KIAA0

						543
1268	AB011161	2.57E-08	4.01E-09	9.64E-11	0.63432	PIP5K1C
1269	AB014535	1.37E-05	5.05E-07	1.04E-06	0.285282	KIAA0635
1270	AB014538	0.0003443	4.67E-05	1.98E-06	-0.63923	KIAA0638
1271	AB014579	1.37E-05	5.01E-06	6.08E-08	0.367966	MGEA5
1272	AB014608	7.44E-05	9.64E-05	4.59E-06	0.41494	KIAA0708
1273	AB015019	7.44E-05	7.05E-06	2.75E-07	-0.24515	BAIAP2
1274	AB018343	1.84E-09	4.16E-10	9.05E-12	0.383078	KIAA0800
1275	AB023153	2.11E-06	1.33E-07	1.82E-08	0.895842	KIAA0936
1276	AB023235	7.44E-05	1.61E-06	1.43E-05	0.311216	KIAA1018
1277	AB026118	0.0013772	0.0001897	4.47E-06	-0.24886	MALT1
1278	AB026436	7.44E-05	1.61E-06	0.000219	-0.7589	DUSP10
1279	AB028951	2.64E-07	1.72E-07	8.78E-09	0.543028	KIAA1028
1280	AB028981	2.11E-06	7.73E-07	5.34E-07	0.282288	KIAA1058
1281	AB029015	2.64E-07	2.49E-07	5.37E-09	0.695063	PLCE2
1282	AB029038	7.44E-05	1.61E-06	7.62E-05	0.364386	KIAA1115
1283	AC002400	1.37E-05	3.06E-05	2.28E-06	-0.25834	UBPH
1284	AF000545	7.44E-05	5.23E-05	3.48E-06	-0.85393	P2Y10
1285	AF001294	1.37E-05	7.05E-06	1.23E-06	-0.76359	TSSC3
1286	AF004230	2.64E-07	1.72E-07	3.06E-07	0.349166	LILRB1
1287	AF005043	7.44E-05	5.23E-05	2.70E-06	0.408592	PARG
1288	AF007130	2.11E-06	5.05E-07	2.51E-06	0.391811	LOC54104
1289	AF007142	0.0003443	0.0004443	3.15E-06	0.678734	
1290	AF007151	1.37E-05	5.05E-07	3.25E-06	0.468343	MMS19L
1291	AF010193	7.44E-05	2.35E-05	1.26E-07	-1.4705	MADH7
1292	AF010309	1.37E-05	5.01E-06	7.36E-07	-0.28533	PIG3
1293	AF012023	7.44E-05	5.92E-05	1.02E-06	0.50623	ICAP-1A
1294	AF014958	2.11E-06	4.31E-06	1.05E-07	-0.42152	CCRL2
1295	AF015553	2.11E-06	9.54E-07	2.61E-07	0.61214	GTF2I
1296	AF019083	1.37E-05	5.01E-06	8.34E-07	0.17011	PTENP1
1297	AF022375	2.64E-07	8.23E-08	1.87E-11	-1.35847	VEGF
1298	AF023614	1.37E-05	1.51E-05	4.79E-07	-0.20744	TACI
1299	AF024710	8.55E-11	8.55E-11	1.13E-12	-1.95537	VEGF

1300	AF026086	0.0003443	4.67E-05	2.66E-06	0.297942	PEX1
1301	AF029777	1.37E-05	7.05E-06	8.27E-07	0.290159	GCN5L2
1302	AF030249	1.37E-05	1.61E-06	1.98E-07	0.534547	ECH1
1303	AF035281	2.11E-06	2.48E-06	4.87E-07	0.472445	
1304	AF038564	1.37E-05	1.61E-06	2.05E-07	-0.40446	ITCH
1305	AF040707	2.11E-06	1.99E-06	3.57E-07	0.289845	NPR2L
1306	AF042386	1.37E-05	5.01E-06	0.000107	0.137192	PPIE
1307	AF052160	7.44E-05	1.51E-05	1.67E-06	0.623021	
1308	AF054176	2.11E-06	1.33E-07	6.47E-09	-0.58138	C1orf7
1309	AF054589	0.0003443	2.35E-05	1.98E-06	0.945394	
1310	AF061258	7.44E-05	9.64E-05	1.58E-06	0.622201	LIM
1311	AF067853	1.37E-05	5.01E-06	5.02E-06	0.361707	ADSL
1312	AF069517	2.11E-06	1.33E-07	4.91E-07	0.399638	RBM6
1313	AF070582	2.64E-07	1.72E-07	3.23E-08	-0.19773	MGC13033
1314	AF070606	1.37E-05	3.06E-05	1.48E-06	-0.89337	
1315	AF070617	1.37E-05	3.86E-06	3.23E-07	0.323494	
1316	AF077820	2.64E-07	2.19E-08	2.91E-08	0.656852	LRP5
1317	AF079167	2.64E-07	2.49E-07	7.37E-10	-1.93249	OLR1
1318	AF082557	0.0013772	4.67E-05	2.23E-06	0.226994	TNKS
1319	AF094481	1.37E-05	5.01E-06	2.74E-07	-0.29045	CGGBP1
1320	AF098641	2.64E-07	1.72E-07	1.56E-07	-0.41172	
1321	AF110377	1.37E-05	5.01E-06	3.05E-05	0.361232	TRRAP
1322	AF117829	7.44E-05	0.000129	2.61E-06	-0.57516	RIPK2
1323	AI133727	7.44E-05	0.0001187	1.43E-06	0.181464	FLB6421
1324	AI141670	0.0003443	0.0003041	1.60E-06	-0.2494	CLCN2
1325	AI148772	0.0003443	4.67E-05	4.18E-06	-1.02619	KYNU
1326	AI184802	2.64E-07	2.19E-08	2.67E-09	-0.21576	HPRP4P
1327	AI560890	2.57E-08	2.83E-08	1.80E-07	0.179028	
1328	AI670100	7.44E-05	2.58E-05	7.70E-07	0.22677	GRLF1
1329	AI754391	1.37E-05	3.86E-06	1.72E-06	-0.27657	KLF12
1330	AI935146	0.0003443	2.35E-05	2.05E-06	-0.46726	GALNT3
1331	AI950382	1.37E-05	1.61E-06	1.63E-07	-0.74128	KIAA0585
1332	AI970189	0.0003443	2.35E-05	6.16E-07	-0.75934	KIAA0997
1333	AJ002190	7.44E-05	1.61E-06	2.17E-08	0.33775	GNPAT
1334	AJ007042	2.64E-07	1.72E-07	2.10E-07	0.170935	WHSC1
1335	AJ010059	2.11E-06	5.05E-07	2.95E-06	0.2235	SIT
1336	AL008583	2.64E-07	2.19E-08	1.12E-08	0.250082	CBX6
1337	AL021154	0.0003443	4.67E-05	2.19E-06	-0.82935	ID3
1338	AL021707	0.0003443	7.05E-06	4.95E-06	-2.21462	
1339	AL022398	7.44E-05	1.61E-06	8.09E-08	0.919627	

1340	AL022398	7.44E-05	7.05E-06	1.10E-07	0.79713	DJ434O14.3
1341	AL022398	7.44E-05	2.58E-05	2.40E-06	0.493166	
1342	AL023553	1.37E-05	1.75E-05	2.51E-06	0.226635	PMM1
1343	AL049387	0.0013772	0.0001897	5.12E-06	0.379296	
1344	AL049409	7.44E-05	1.51E-05	1.10E-06	0.714173	LEF1
1345	AL049782	7.44E-05	2.58E-05	7.66E-07	0.237794	
1346	AL049787	1.37E-05	5.01E-06	7.11E-06	0.311278	
1347	AL049963	0.0003443	4.67E-05	8.36E-07	-0.74421	LOC64116
1348	AL050084	7.44E-05	1.61E-06	5.26E-05	0.509331	DC8
1349	AL050087	2.11E-06	2.48E-06	1.27E-07	-0.31279	KIAA1785
1350	AL050196	1.37E-05	5.01E-06	2.00E-05	-0.24688	DKFZP586D2223
1351	AL050281	0.0003443	0.0002051	2.85E-06	0.30517	NAG
1352	AL050353	0.0003443	2.35E-05	4.42E-06	0.179352	OIP2
1353	AL050371	0.0003443	2.35E-05	3.70E-06	0.493288	PISD
1354	AL080071	0.0003443	0.0003041	3.12E-06	0.237367	DKFZP564M082
1355	AL080141	1.37E-05	5.01E-06	2.42E-07	0.330868	SEC31B-1
1356	AL096780	1.37E-05	5.05E-07	2.13E-06	0.34487	CHKL
1357	AW051579	1.37E-05	1.61E-06	7.58E-07	0.593476	FLJ10512
1358	D10704	1.37E-05	1.75E-05	4.69E-07	-0.36791	CHK
1359	D13891	2.11E-06	2.48E-06	4.57E-05	-0.20577	ID2
1360	D30758	2.11E-06	1.99E-06	1.58E-05	0.27738	CENTB1
1361	D30783	2.57E-08	2.83E-08	8.95E-10	-1.65011	EREG
1362	D49677	7.44E-05	7.05E-06	4.18E-06	0.198707	U2AF1RS2
1363	D50406	1.37E-05	3.86E-06	2.65E-05	0.461907	RECK
1364	D50525	0.0003443	4.67E-05	3.02E-06	0.486698	
1365	D78579	1.37E-05	7.05E-06	4.25E-07	-1.65638	NR4A3
1366	D78579	7.44E-05	7.05E-06	9.62E-07	-1.61438	NR4A3
1367	D80011	7.44E-05	1.61E-06	4.20E-07	-0.35073	KIAA0189
1368	D87119	7.44E-05	2.35E-05	1.80E-06	0.425625	GS3955
1369	D87119	7.44E-05	5.23E-05	4.62E-06	0.557116	GS3955
1370	D87466	1.37E-05	8.66E-06	1.49E-07	0.466046	KIAA0276
1371	HG1103-HT1103	1.37E-05	1.61E-06	1.16E-07	-0.39165	
1372	HG2007-HT2056	7.44E-05	9.64E-05	4.01E-06	-0.41408	
1373	HG2724-HT2820	1.37E-05	3.06E-05	5.17E-06	-1.33814	
1374	HG3227-	2.64E-07	1.72E-07	1.68E-08	-0.25361	

	HT3404					
1375	HG4582-HT4987	7.44E-05	2.35E-05	4.63E-07	-0.39588	
1376	J02939	7.44E-05	1.61E-06	2.16E-07	-0.87844	SLC3A2
1377	J02973	1.37E-05	5.05E-07	2.93E-07	-1.30804	THBD
1378	J03258	0.0003443	0.0001695	1.21E-06	-0.58295	VDR
1379	J04130	0.0003443	2.35E-05	3.02E-06	-0.62071	SCYA4
1380	L04733	0.0013772	2.35E-05	8.84E-07	0.306455	KNS2
1381	L05424	2.11E-06	1.33E-07	2.27E-09	-0.58081	CD44
1382	L12002	7.44E-05	4.67E-05	1.23E-06	0.286717	ITGA4
1383	L13740	2.64E-07	2.19E-08	5.83E-08	-1.45891	NR4A1
1384	L13740	1.37E-05	5.01E-06	9.10E-08	-0.61928	NR4A1
1385	L13773	1.37E-05	1.75E-05	6.44E-07	0.247919	MLLT2
1386	L16499	1.37E-05	8.66E-06	5.12E-06	0.374296	HHEX
1387	L20941	2.64E-07	1.33E-07	1.78E-06	-0.58618	FTH1
1388	L22075	2.64E-07	2.49E-07	1.10E-08	-0.55736	GNA13
1389	L22569	1.37E-05	8.66E-06	1.52E-06	0.318129	CTSB
1390	L25665	0.0003443	0.0001695	3.34E-06	-0.4513	GNL1
1391	L33881	2.64E-07	1.72E-07	5.06E-08	-0.59585	PRKCI
1392	L40377	1.37E-05	5.05E-07	3.49E-07	-0.79409	SERPINB8
1393	L47738	2.57E-08	4.01E-09	7.54E-09	0.31646	PIR121
1394	L78132	7.44E-05	5.23E-05	5.15E-07	0.358576	LGALS8
1395	M12267	0.0003443	0.0001695	4.07E-06	-0.3279	OAT
1396	M12959	7.44E-05	2.58E-05	1.61E-06	0.128482	TRA@
1397	M15330	8.55E-11	8.55E-11	2.49E-12	-2.13825	IL1B
1398	M17017	7.44E-05	0.0001187	1.43E-06	-1.74073	IL8
1399	M22919	2.64E-07	3.12E-07	9.52E-08	-0.81053	MYL6
1400	M23114	2.11E-06	4.31E-06	1.59E-07	-0.96141	ATP2A2
1401	M24194	7.44E-05	1.61E-06	4.38E-06	0.560895	GNB2L1
1402	M24283	0.0003443	4.67E-05	3.71E-06	-1.32611	ICAM1
1403	M24895	2.11E-06	1.33E-07	1.72E-08	0.476779	AMY2B
1404	M26683	7.44E-05	0.0001187	3.70E-06	-0.16179	SCYA2
1405	M27492	0.0003443	0.0004017	2.01E-06	-0.32619	IL1R1
1406	M28130	7.44E-05	4.67E-05	8.02E-07	-2.27292	IL8
1407	M31165	7.44E-05	5.23E-05	1.38E-06	-0.34617	TNFAIP6
1408	M31523	1.37E-05	1.75E-05	2.09E-06	0.36898	TCF3
1409	M36821	1.37E-05	8.66E-06	2.21E-07	-0.36334	GRO3
1410	M55153	7.44E-05	2.58E-05	4.77E-06	-0.27465	TGM2
1411	M58603	7.44E-05	5.23E-05	1.28E-06	-0.73537	NFKB1
1412	M59040	0.0013772	2.35E-05	2.82E-06	-0.46271	CD44
1413	M60784	7.44E-05	5.23E-05	1.24E-06	0.559903	SNRPA
1414	M60922	7.44E-05	1.51E-05	4.47E-08	0.39657	FLOT2

1415	M62403	7.44E-05	5.23E-05	5.57E-07	-0.53749	IGFBP 4
1416	M63256	0.0003443	5.92E-05	6.54E-07	0.454561	CDR2
1417	M63904	2.57E-08	1.03E-08	5.38E-09	-0.59612	GNA15
1418	M63978	0.0003443	4.67E-05	1.77E-06	-0.44762	VEGF
1419	M64571	1.84E-09	1.84E-09	2.41E-11	0.416659	MAP4
1420	M69199	2.11E-06	1.99E-06	1.45E-07	-1.9021	G0S2
1421	M73547	1.37E-05	5.01E-06	9.20E-08	0.438897	D5S346
1422	M74525	2.11E-06	2.48E-06	3.50E-07	-0.61792	UBE2B
1423	M80244	0.0003443	7.05E-06	2.72E-06	-0.8522	SLC7A 5
1424	M84443	1.37E-05	5.05E-07	4.08E-07	0.303567	GALK2
1425	M94856	7.44E-05	5.23E-05	4.99E-06	-0.23847	FABP5
1426	M95678	0.0003443	7.05E-06	2.00E-06	0.432923	PLCB2
1427	M98833	7.44E-05	1.61E-06	1.52E-06	0.434288	FLI1
1428	N23137	2.11E-06	2.48E-06	2.06E-07	0.247311	MPHO SPH9
1429	N23137	0.0013772	0.0001695	4.12E-06	0.244083	MPHO SPH9
1430	N30151	7.44E-05	1.61E-06	5.05E-05	0.393521	STX16
1431	N42007	2.11E-06	2.48E-06	9.19E-05	0.167986	NUP50
1432	N53547	7.44E-05	8.56E-05	1.80E-07	0.296678	MGC55 08
1433	N90862	1.37E-05	5.05E-07	3.28E-08	0.43576	VAMP 8
1434	N90866	2.64E-07	8.23E-08	2.76E-08	0.304525	CDW52
1435	N98667	1.37E-05	8.66E-06	3.38E-07	0.367127	KIAA1 696
1436	R90942	1.37E-05	5.01E-06	1.05E-05	-0.17696	ST6GA LNACI V
1437	S52028	2.11E-06	5.05E-07	9.62E-08	-0.81662	CTH
1438	S68134	0.0003443	7.05E-06	8.37E-07	-1.64652	CREM
1439	S68134	0.0003443	7.05E-06	4.35E-06	-2.47105	CREM
1440	S68271	0.0003443	7.05E-06	3.03E-06	-2.07185	CREM
1441	S73591	1.37E-05	1.51E-05	4.68E-06	0.414777	VDUP1
1442	S76638	7.44E-05	2.35E-05	7.47E-07	-0.35416	NFKB2
1443	S78187	7.44E-05	1.61E-06	1.95E-05	0.203265	CDC25 B
1444	S78771	0.0003443	5.92E-05	2.55E-06	-0.31389	BRD2
1445	S81914	0.0003443	7.05E-06	4.18E-07	-1.59146	IER3
1446	U02020	1.37E-05	8.66E-06	1.37E-06	-1.13863	PBEF
1447	U02570	1.37E-05	2.81E-05	1.26E-06	0.432431	ARHG AP1
1448	U03634	1.37E-05	1.75E-05	1.00E-06	-0.21467	LBC
1449	U04636	0.0003443	5.92E-05	2.81E-06	-1.85123	PTGS2
1450	U05681	7.44E-05	5.23E-05	3.37E-06	-0.35383	BCL3
1451	U07563	7.44E-05	2.35E-05	4.91E-07	-0.25016	ABL1
1452	U09937	1.84E-09	4.16E-10	2.04E-09	-1.21578	PLAUR

1453	U10117	7.44E-05	1.51E-05	4.07E-06	0.563673	SCYE1
1454	U11732	1.37E-05	3.86E-06	3.04E-07	-0.22574	ETV6
1455	U12767	7.44E-05	1.61E-06	2.84E-07	-1.23483	NR4A3
1456	U12767	0.0003443	7.05E-06	2.55E-07	-2.13744	NR4A3
1457	U13695	7.44E-05	1.61E-06	1.11E-05	0.805607	PMS1
1458	U15552	1.37E-05	5.01E-06	1.67E-05	-0.68094	HSU15552
1459	U17760	0.0003443	7.05E-06	4.25E-06	-0.84472	LAMB3
1460	U18300	7.44E-05	0.000129	2.43E-06	0.183171	DDB2
1461	U20982	2.11E-06	1.99E-06	1.20E-08	-0.67125	IGFBP4
1462	U24166	7.44E-05	1.61E-06	7.52E-06	-0.45293	MAPRE1
1463	U28811	0.0003443	7.05E-06	1.33E-06	0.32855	GLG1
1464	U29171	1.37E-05	5.01E-06	1.10E-06	-0.6032	CSNK1D
1465	U29175	1.37E-05	8.66E-06	1.90E-06	0.266342	SMARCA4
1466	U29185	2.11E-06	7.73E-07	1.56E-07	-1.08006	PRNP
1467	U29344	2.11E-06	9.54E-07	2.35E-07	-0.43842	FASN
1468	U29656	2.11E-06	7.73E-07	7.52E-08	0.353186	NME3
1469	U29656	7.44E-05	0.000129	4.31E-06	0.471876	NME3
1470	U32324	1.37E-05	5.05E-07	3.21E-08	0.334966	IL11RA
1471	U33017	2.64E-07	1.72E-07	5.20E-07	0.373581	SLAM
1472	U38847	7.44E-05	2.35E-05	9.91E-07	0.222946	TARBP1
1473	U41815	1.37E-05	5.05E-07	2.16E-07	-0.96931	NUP98
1474	U43774	0.0003443	2.35E-05	8.80E-07	-0.39938	FCAR
1475	U44839	2.11E-06	9.54E-07	2.54E-07	-0.97008	USP11
1476	U47414	2.11E-06	9.54E-07	2.31E-06	0.370736	CCNG2
1477	U47927	2.57E-08	2.83E-08	5.53E-09	0.545592	USP5
1478	U48807	1.37E-05	5.01E-06	4.97E-08	-0.93178	DUSP4
1479	U49187	7.44E-05	1.51E-05	1.48E-06	0.671467	C6orf32
1480	U49187	7.44E-05	9.64E-05	3.53E-06	0.511392	C6orf32
1481	U49844	7.44E-05	7.05E-06	3.67E-07	0.47168	ATR
1482	U50527	1.37E-05	5.01E-06	5.11E-06	0.416543	
1483	U50928	7.44E-05	1.61E-06	4.72E-06	0.302213	PKD2
1484	U51007	7.44E-05	1.51E-05	1.49E-06	0.309996	PSMD4
1485	U51205	1.37E-05	5.05E-07	2.65E-07	-0.76279	COP9
1486	U51478	7.44E-05	2.35E-05	6.10E-07	-0.58	ATP1B3
1487	U51920	2.11E-06	1.33E-07	7.01E-08	-0.28142	SRP54
1488	U52960	2.11E-06	1.61E-06	1.51E-07	-0.84863	SURB7
1489	U56998	0.0003443	7.05E-06	3.70E-06	-0.74294	CNK
1490	U64197	1.84E-09	1.84E-09	2.95E-10	-0.62373	SCYA20
1491	U65928	7.44E-05	4.67E-05	2.85E-07	0.408918	COPS5
1492	U66063	2.11E-06	2.48E-06	4.70E-07	0.277185	CAMK

						2G
1493	U70735	1.37E-05	8.66E-06	1.82E-06	0.249185	MOV34-34KD
1494	U72066	2.57E-08	1.03E-08	4.33E-08	-0.34482	RBBP8
1495	U75968	2.11E-06	1.99E-06	4.36E-06	0.139542	DDX11
1496	U78107	8.55E-11	3.69E-11	4.04E-12	-0.43769	NAPG
1497	U78302	2.64E-07	1.72E-07	2.41E-08	0.329878	DECR1
1498	U78798	2.57E-08	4.01E-09	1.11E-06	-0.3172	TRAF6
1499	U84007	7.44E-05	1.61E-06	0.000235	0.236422	AGL
1500	U85245	7.44E-05	1.61E-06	4.57E-07	0.365266	PIP5K2B
1501	U88629	0.0003443	4.67E-05	9.58E-07	-0.32607	ELL2
1502	U90917	1.37E-05	1.61E-06	3.89E-07	0.433406	FOXM1
1503	U91543	2.64E-07	3.12E-07	2.01E-07	0.478678	CHD3
1504	U91616	1.37E-05	5.05E-07	1.27E-07	-0.80419	NFKBIE
1505	U96876	7.44E-05	1.61E-06	3.54E-06	-0.45317	INSIG1
1506	U97105	1.37E-05	1.75E-05	6.56E-07	1.00615	DPYSL2
1507	W28319	1.37E-05	5.01E-06	1.50E-05	0.294631	FBLN1
1508	W28612	1.37E-05	5.01E-06	1.70E-06	-0.25519	
1509	W28743	0.0003443	7.05E-06	2.78E-06	-0.28926	PP1628
1510	X00737	2.11E-06	9.54E-07	5.21E-08	-0.67074	NP
1511	X02152	1.37E-05	5.05E-07	4.63E-08	-0.75601	LDHA
1512	X04366	1.37E-05	2.81E-05	5.11E-06	0.346076	CAPN1
1513	X04500	2.64E-07	1.72E-07	3.43E-10	-2.12121	IL1B
1514	X06256	1.37E-05	2.35E-05	4.89E-07	-0.7357	ITGA5
1515	X13403	7.44E-05	5.92E-05	4.21E-07	0.146032	POU2F1
1516	X15217	7.44E-05	4.67E-05	3.77E-07	-0.2371	SKIL
1517	X15218	8.55E-11	8.55E-11	1.40E-10	-1.41501	SKI
1518	X16396	0.0003443	0.0002051	3.27E-06	-0.6151	MTHFD2
1519	X16706	7.44E-05	1.61E-06	1.23E-06	-1.09747	FOSL2
1520	X53586	1.37E-05	8.66E-06	3.40E-07	0.51291	ITGA6
1521	X58141	7.44E-05	9.64E-05	1.75E-06	0.384254	ADD1
1522	X61123	7.44E-05	0.0001057	4.17E-07	-1.15256	BTG1
1523	X61498	7.44E-05	1.61E-06	8.80E-07	-0.49884	NFKB2
1524	X62535	1.37E-05	1.61E-06	5.68E-07	0.243937	DGKA
1525	X63368	2.11E-06	5.05E-07	2.30E-08	-0.55432	DNAJB2
1526	X64330	7.44E-05	7.05E-06	2.27E-06	0.297851	ACLY
1527	X66363	2.64E-07	1.72E-07	6.53E-07	-0.24505	PCTK1
1528	X66436	0.0003443	8.56E-05	1.88E-06	-0.26662	
1529	X66945	7.44E-05	1.51E-05	1.91E-07	-0.35494	FGFR1
1530	X68452	2.57E-08	4.01E-09	9.12E-11	-0.26618	CCND2
1531	X69392	2.64E-07	1.33E-07	1.10E-08	0.297444	RPL26
1532	X70218	1.37E-05	3.06E-05	2.44E-06	-0.74691	PPP4C

1533	X74039	1.84E-09	4.16E-10	1.51E-10	-0.67381	PLAUR
1534	X79882	1.37E-05	5.05E-07	1.78E-07	0.520965	MVP
1535	X82153	7.44E-05	1.61E-06	2.27E-06	0.47844	CTSK
1536	X82209	2.11E-06	5.05E-07	1.37E-09	-0.45281	MN1
1537	X87949	7.44E-05	1.61E-06	4.05E-07	-0.54468	HSPA5
1538	X98172	7.44E-05	4.67E-05	5.29E-07	0.507556	CASP8
1539	X99142	1.37E-05	8.66E-06	1.24E-06	-0.29773	KRTHB6
1540	X99656	1.37E-05	5.05E-07	1.68E-06	-0.23553	SH3GL1
1541	Y00630	2.57E-08	3.70E-08	6.65E-09	-2.38485	SERPINB2
1542	Y08683	1.37E-05	5.05E-07	4.71E-06	0.492738	CPT1B
1543	Y14768	1.37E-05	5.05E-07	7.26E-08	0.248383	LTB
1544	Y18004	1.37E-05	5.01E-06	4.19E-07	-0.9465	SCML2
1545	Z11697	1.37E-05	5.05E-07	3.55E-06	-1.21033	CD83
1546	Z14000	0.0003443	0.0002051	3.91E-06	-0.33734	RING1
1547	Z24724	2.64E-07	2.19E-08	5.96E-09	-1.10426	
1548	Z32860	1.37E-05	5.01E-06	7.81E-06	0.133192	
1549	Z93930	2.64E-07	2.49E-07	2.42E-05	-0.39839	XBP1

Table III: Differential Gene Expression in acute MS relapse vs. remission

SEQ ID NO:	Identifier	TNOM PValue	Info PValue	t-Test PValue	Log Fold Change	Symbol
1550	AI828210	5.38E-06	5.38E-06	8.37E-06	-0.18947	KIAA0284
1551	D14710	6.73E-05	3.19E-05	2.89E-05	-0.35496	ATP5A1
1552	U46692	6.73E-05	3.19E-05	0.000284	-0.49741	CSTB
1553	AF061261	6.73E-05	3.19E-05	3.22E-05	-0.28274	MBLL
1554	U51712	6.73E-05	3.19E-05	0.003464	-0.42775	SMAP31
1555	AB014558	6.73E-05	4.25E-05	0.000473	0.694784	CRY2
1556	AB007936	6.73E-05	4.25E-05	0.000958	-0.25409	KIAA0467
1557	AC002115	6.73E-05	4.25E-05	0.000147	0.622841	MGC10433
1558	AF052160	6.73E-05	4.25E-05	0.000182	-0.46468	
1559	S78085	0.000538	0.000104	0.000102	-0.55064	PDCD2
1560	AL096719	0.000538	0.000104	0.000089	-0.22287	PFN2
1561	U61234	0.000538	0.000104	0.000844	0.299182	TBCC
1562	X12451	0.000538	0.000251	0.000876	1.04444	CTSL
1563	M35531	0.000538	0.000251	0.000241	-0.20303	FUT1
1564	M64174	0.000538	0.000251	3.43E-05	-0.5508	JAK1
1565	AB018269	0.000538	0.000251	7.39E-05	-0.18186	KIAA0726
1566	R92331	0.000538	0.000251	0.000104	0.289994	MT1E
1567	U19487	0.000538	0.000251	0.001738	-0.25888	PTGER2
1568	AF040965	0.000538	0.000251	0.000775	0.48898	RES4-25
1569	U07563	0.000538	0.000251	3.61E-05	-0.16779	RRP4
1570	L40377	0.000538	0.000251	0.009479	0.452416	SERPINB8
1571	AL080234	0.000538	0.000251	0.000377	-0.52631	

1572	AJ242015	0.003096	0.00039	0.013957	0.281618	ADAM28
1573	D86324	0.003096	0.00039	0.001801	-0.34728	CMAH
1574	M94065	0.003096	0.00039	0.002391	-0.13976	DHODH
1575	AC004382	0.003096	0.00039	0.000121	-0.20383	DKFZP434K046
1576	X54326	0.003096	0.00039	0.002734	-0.39559	EPRS
1577	W25921	0.003096	0.00039	9.41E-05	-0.39027	GNS
1578	X92110	0.003096	0.00039	0.000103	-1.00581	HCGVIII-1
1579	W28589	0.003096	0.00039	0.000225	-0.20949	HSPD1
1580	S66213	0.003096	0.00039	0.000134	-0.28606	ITGA6
1581	AB011158	0.000538	0.00039	0.000047	-0.163	KIAA0586
1582	AB023209	0.003096	0.00039	0.003354	-0.09151	KIAA0992
1583	AF035940	0.003096	0.00039	0.008457	0.282437	MAGOH
1584	M31724	0.003096	0.00039	0.000671	0.569343	PTPN1
1585	X74262	0.003096	0.00039	0.000062	-0.37623	RBBP4
1586	J05249	0.003096	0.00039	0.00045	-0.52346	RPA2
1587	M55531	0.003096	0.00039	0.023054	-0.22329	SLC2A5
1588	AI865431	0.003096	0.00039	0.00027	0.423067	TNFRSF5
1589	W28203	0.003096	0.00039	0.007983	-0.17484	
1590	W28667	0.003096	0.00039	0.000846	-0.49488	
1591	D13628	0.000538	0.000529	0.034335	-0.10398	ANGPT1
1592	U03271	0.000538	0.000529	0.000286	-0.1675	CAPZB
1593	U05259	0.000538	0.000529	0.003589	0.551328	CD79A
1594	L13278	0.000538	0.000529	7.27E-05	-0.43636	CRYZ
1595	M91670	0.000538	0.000529	0.003472	0.600255	E2-EPF
1596	AB029030	0.000538	0.000529	0.000657	-0.13458	KIAA1107
1597	AF016098	0.000538	0.000529	0.000433	-0.16189	NRP2
1598	X76091	0.000538	0.000529	0.004691	0.161349	RFX2
1599	U52191	0.000538	0.000529	0.00229	1.2356	SMCY
1600	AA203345	0.000538	0.000529	0.001228	-0.50409	STX16
1601	U96113	0.000538	0.000529	0.000394	-0.41425	WWP1
1602	AL050263	0.000538	0.000529	0.000224	-0.15981	
1603	Z48579	0.000538	0.000799	0.000184	-0.30836	ADAM10
1604	M31452	0.000538	0.000799	0.002899	-0.13022	C4BPA
1605	AC003107	0.000538	0.000799	0.000262	-0.16818	COMP
1606	M91670	0.000538	0.000799	0.000792	0.41925	E2-EPF
1607	AB023235	0.000538	0.000799	0.001348	-0.30138	KIAA1018
1608	X89960	0.000538	0.000799	0.026837	-0.35169	MCSP
1609	D55654	0.000538	0.000799	0.019331	-0.2254	MDH1
1610	U02683	0.000538	0.000799	0.030035	-0.09324	NRF1
1611	S90469	0.000538	0.000799	0.000785	0.23032	POR
1612	AF020543	0.000538	0.000799	0.004286	-0.25061	PPT2
1613	M34181	0.000538	0.000799	0.000055	-0.5883	PRKACB
1614	AF095448	0.000538	0.000799	0.000588	-0.24961	RAI3
1615	AF027150	0.000538	0.000799	0.000979	-0.16012	SIP1
1616	X02344	0.000538	0.000799	0.000918	0.430531	TUBB2
1617	X02344	0.000538	0.000799	0.002225	0.296682	TUBB2

1618	AI701164	0.000538	0.000799	0.000115	-0.23639	UBE2G1
1619	U96113	0.000538	0.000799	9.77E-05	-0.45711	WWP1
1620	AF016052	0.000538	0.000799	0.001254	-0.19092	ZNF24
1621	U21551	0.003096	0.00103	0.000836	0.278219	BCAT1
1622	X77794	0.003096	0.00103	3.72E-05	-0.81938	CCNG1
1623	AF070530	0.003096	0.00103	0.014908	0.276942	CL24751
1624	AB002331	0.003096	0.00103	0.001714	-0.17304	DATF1
1625	AI004207	0.003096	0.00103	0.000762	-0.1648	FLJ00002
1626	L76200	0.003096	0.00103	0.000824	0.444479	GUK1
1627	U26398	0.003096	0.00103	0.001182	-0.29185	INPP4A
1628	U69883	0.003096	0.00103	0.007922	0.103614	KCNN1
1629	M13452	0.003096	0.00103	0.000467	0.405856	LMNA
1630	AA126505	0.003096	0.00103	0.002	-0.39781	NCAM1
1631	U88620	0.003096	0.00103	0.007562	-0.3532	OGG1
1632	M33336	0.003096	0.00103	0.001568	-0.26454	PRKAR1A
1633	AB015982	0.003096	0.00103	0.000382	-0.27486	PRKCN
1634	H68340	0.003096	0.00103	0.001222	0.516352	RNAHP
1635	M28225	0.003096	0.00103	0.000686	1.0733	SCYA2
1636	X97064	0.003096	0.00103	0.003207	-0.19906	SEC23A
1637	X68560	0.003096	0.00103	0.007856	0.437567	SP3
1638	AF064094	0.003096	0.00103	0.000287	-0.19385	TADA2L
1639	AB007872	0.003096	0.00103	0.000119	-0.20778	ZNF264
1640	W28255	0.013622	0.001698	0.001407	-0.24426	76P
1641	AB007934	0.003096	0.001698	0.003182	-0.24405	ACF7
1642	AL049954	0.013622	0.001698	0.024193	-0.25818	AHCYL1
1643	U90546	0.003096	0.001698	0.000105	-0.34074	BTN3A2
1644	AL035291	0.013622	0.001698	0.007668	0.506107	CH1
1645	AF031647	0.013622	0.001698	0.004755	0.257244	COPS3
1646	M57888	0.003096	0.001698	0.004549	-0.64384	CTLA1
1647	AF000987	0.003096	0.001698	0.009455	0.247586	EIF1AY
1648	U55766	0.003096	0.001698	0.00066	0.795017	HRB2
1649	L12002	0.013622	0.001698	0.005765	-0.1942	ITGA4
1650	D14661	0.013622	0.001698	0.011324	0.391267	KIAA0105
1651	D63875	0.013622	0.001698	0.002192	-0.36411	KIAA0155
1652	AB018285	0.013622	0.001698	0.001545	0.550994	KIAA0742
1653	AB023180	0.013622	0.001698	0.001642	0.253479	KIAA0963
1654	AL080102	0.013622	0.001698	0.003651	0.435751	KIAA1856
1655	M22637	0.013622	0.001698	0.003792	-0.27794	LYL1
1656	D85131	0.013622	0.001698	0.005126	-0.12291	MAZ
1657	D37965	0.013622	0.001698	0.01111	-0.09143	PDGFRL
1658	Y18207	0.003096	0.001698	0.003474	-0.17238	PPP1R3C
1659	L49229	0.013622	0.001698	0.000336	-0.36639	RB1
1660	U77664	0.013622	0.001698	0.002354	0.193666	RPP38
1661	AL040137	0.003096	0.001698	0.008384	-0.23366	SAP18
1662	D31764	0.013622	0.001698	0.01295	-0.13299	SNX17
1663	X57655	0.013622	0.001698	0.002476	-0.17382	SPINK2

1664	M19267	0.013622	0.001698	0.013582	0.262886	TPM1
1665	M12959	0.013622	0.001698	0.003907	-0.08942	TRA@
1666	AA160724	0.013622	0.001698	0.005695	0.267002	
1667	U37122	0.003096	0.002135	0.000571	-0.59281	ADD3
1668	AA903720	0.003096	0.002135	0.002557	0.244618	BAP29
1669	M93107	0.003096	0.002135	0.00187	-0.19146	BDH
1670	M17754	0.003096	0.002135	0.010333	-0.10769	BN51T
1671	X15882	0.003096	0.002135	0.0023	0.227769	COL6A2
1672	D15057	0.003096	0.002135	0.002814	-0.26776	DAD1
1673	S62138	0.003096	0.002135	0.002442	1.1158	DDIT3
1674	AB026436	0.003096	0.002135	0.011189	0.711919	DUSP10
1675	W27152	0.003096	0.002135	0.009498	-0.1614	FLJ10569
1676	AB001106	0.003096	0.002135	0.002408	0.444617	GMFB
1677	D87120	0.003096	0.002135	0.00475	0.236706	GS3786
1678	AI200373	0.003096	0.002135	0.003822	-0.31066	H2AFI
1679	U15085	0.003096	0.002135	0.011743	0.328857	HLA-DMB
1680	U90549	0.003096	0.002135	0.001654	-0.26437	HMG17L3
1681	AI760162	0.003096	0.002135	0.001313	-0.47775	HT012
1682	AB018306	0.003096	0.002135	0.000371	0.316202	KIAA0763
1683	D14696	0.003096	0.002135	0.016949	0.259239	LAPTM4A
1684	U23852	0.003096	0.002135	0.001207	-0.2593	LCK
1685	U70735	0.003096	0.002135	0.0002	-0.20846	MOV34-34KD
1686	X79865	0.003096	0.002135	0.0141	0.418466	MRPL12
1687	AI547258	0.003096	0.002135	0.001223	0.267951	MT2A
1688	L40387	0.003096	0.002135	0.00038	0.211973	OASL
1689	AB019517	0.003096	0.002135	0.023004	0.219453	PKIG
1690	M58459	0.003096	0.002135	0.001362	1.46854	RPS4Y
1691	X57348	0.003096	0.002135	0.004255	0.22047	SFN
1692	M74558	0.003096	0.002135	0.001205	0.219185	SIL
1693	U34044	0.003096	0.002135	0.000831	-0.21289	SPS
1694	U49928	0.003096	0.002135	0.000886	-0.31189	TAB1
1695	X05839	0.003096	0.002135	0.008747	0.214552	TGFB1
1696	U16296	0.003096	0.002135	0.006585	-0.14857	TIAM1
1697	U63127	0.003096	0.002135	0.000538	-0.38925	TIC
1698	U03397	0.003096	0.002135	0.005156	-0.34157	TNFRSF9
1699	M21624	0.003096	0.002135	0.001748	-0.51878	TRD@
1700	D83198	0.003096	0.002135	0.028975	-0.17519	YF13H12
1701	HG960-HT960	0.003096	0.002135	0.003089	0.145701	
1702	HG4724-HT5166	0.003096	0.002135	0.002446	-0.25728	
1703	D00654	0.003096	0.004342	9.79E-05	-0.1819	ACTG2
1704	U54645	0.013622	0.004342	0.004228	-0.25281	AK2
1705	M93405	0.003096	0.004342	0.020651	0.126156	ALDH6A1
1706	U73960	0.003096	0.004342	0.002279	0.555806	ARL4
1707	U26455	0.003096	0.004342	0.006562	-0.53911	ATM
1708	M33519	0.003096	0.004342	0.011169	-0.33327	BAT3

1709	U90028	0.003096	0.004342	0.000396	-0.24971	BICD1
1710	AB002384	0.003096	0.004342	0.002855	-0.46941	C6orf32
1711	M74093	0.003096	0.004342	0.000763	-0.33022	CCNE1
1712	AA203246	0.003096	0.004342	0.007014	-0.16607	CDC2L5
1713	X66358	0.013622	0.004342	0.007122	-0.1886	CDKL1
1714	U30872	0.003096	0.004342	0.001715	-0.164	CENPF
1715	AB020675	0.013622	0.004342	0.002913	-0.25056	CNTNAP2
1716	M13207	0.013622	0.004342	0.01388	0.122241	CSF2
1717	AA173896	0.013622	0.004342	0.008401	0.305133	CYB5-M
1718	L78267	0.003096	0.004342	0.04708	0.103949	D15S226E
1719	AL080120	0.013622	0.004342	0.001834	-0.12922	DKFZP564O0423
1720	U13896	0.013622	0.004342	0.020482	-0.10291	DLG1
1721	AF034970	0.013622	0.004342	0.010371	-0.10568	DOK2
1722	D12686	0.013622	0.004342	0.003493	0.170378	EIF4G1
1723	AB002386	0.003096	0.004342	0.000131	-0.39255	EZH1
1724	M15059	0.003096	0.004342	0.002497	0.2061	FCER2
1725	W27545	0.013622	0.004342	0.004445	0.379682	FLJ20259
1726	M84443	0.003096	0.004342	0.000101	-0.27085	GALK2
1727	AF029777	0.013622	0.004342	0.001427	-0.22426	GCN5L2
1728	D63876	0.013622	0.004342	0.002737	0.396946	GGA3
1729	AB020645	0.003096	0.004342	0.003907	-0.37377	GLS
1730	U77948	0.003096	0.004342	0.000818	-0.35677	GTF2I
1731	AF035555	0.003096	0.004342	0.018388	-0.17666	HADH2
1732	AF055001	0.003096	0.004342	0.010744	0.724714	HERPUD1
1733	D32129	0.003096	0.004342	0.005364	-0.13287	HLA-A
1734	AF043586	0.003096	0.004342	0.001047	-0.30021	IGL@
1735	U53831	0.013622	0.004342	0.01853	0.488267	IRF7
1736	AB002344	0.003096	0.004342	0.001658	0.705775	KIAA0346
1737	AI677689	0.013622	0.004342	0.004375	-0.1411	KIAA0685
1738	AB023153	0.003096	0.004342	0.04282	-0.39134	KIAA0936
1739	AB023226	0.003096	0.004342	0.000111	-0.71413	KIAA1009
1740	AI148772	0.013622	0.004342	0.03739	0.532454	KYNU
1741	AB006780	0.003096	0.004342	0.010236	0.178362	LGALS3
1742	AL050405	0.003096	0.004342	0.008144	0.311843	LOC51634
1743	L35253	0.013622	0.004342	0.001324	-0.46397	MAPK14
1744	R93527	0.013622	0.004342	0.000372	0.264207	MT1H
1745	AF108145	0.003096	0.004342	0.001206	-0.14877	MYLE
1746	M96980	0.013622	0.004342	0.002106	-0.16409	MYT1
1747	S76638	0.013622	0.004342	0.04529	0.171344	NFKB2
1748	D88674	0.013622	0.004342	0.045232	0.346415	OAZIN
1749	AL050353	0.013622	0.004342	0.016071	-0.11979	OIP2
1750	AL080119	0.003096	0.004342	0.001961	-0.40821	PAI-RBP1
1751	X76770	0.013622	0.004342	0.005011	-0.10613	PAPOLA
1752	D11466	0.003096	0.004342	0.009752	0.738127	PIGA
1753	W28299	0.003096	0.004342	0.001225	-0.17755	PINK1
1754	U83981	0.003096	0.004342	0.014327	0.28747	PPP1R15A

1755	X14968	0.013622	0.004342	0.004727	0.105215	PRKAR2A
1756	M55284	0.003096	0.004342	0.003435	-0.17401	PRKCH
1757	M15036	0.003096	0.004342	0.010965	-0.25119	PROS1
1758	Y00638	0.003096	0.004342	0.004977	-0.30956	PTPRC
1759	Y00815	0.003096	0.004342	0.015344	0.116938	PTPRF
1760	M38258	0.003096	0.004342	0.009252	-0.14193	RARG
1761	AF025654	0.003096	0.004342	0.002302	-0.39122	RNGTT
1762	M60724	0.013622	0.004342	0.004732	-0.22065	RPS6KB1
1763	AB006202	0.013622	0.004342	0.003028	-0.18268	SDHD
1764	AA890010	0.003096	0.004342	0.00546	-0.21285	SEC22L1
1765	X62822	0.003096	0.004342	0.039707	-0.21593	SIAT1
1766	L41680	0.003096	0.004342	0.001771	-0.16486	SIAT8D
1767	X15217	0.003096	0.004342	0.007377	0.149306	SKIL
1768	L13857	0.003096	0.004342	0.005721	-0.11073	SOS1
1769	U09564	0.003096	0.004342	0.001203	-0.27717	SRPK1
1770	Z75330	0.013622	0.004342	0.031796	-0.11359	STAG1
1771	X92762	0.003096	0.004342	0.001021	-0.27946	TAZ
1772	AF064090	0.003096	0.004342	0.006206	0.303013	TNFSF14
1773	U47634	0.003096	0.004342	0.0057	0.278205	TUBB4
1774	L27071	0.003096	0.004342	0.000732	-0.39906	TXK
1775	D78514	0.003096	0.004342	0.000681	-0.2599	UBE2G1
1776	AF085807	0.003096	0.004342	0.005801	0.124457	UPK1A
1777	U66561	0.003096	0.004342	0.002542	0.448044	ZNF184
1778	X78925	0.013622	0.004342	0.001898	0.351929	ZNF267
1779	HG2510-HT2606	0.013622	0.004342	0.007016	0.179499	
1780	W27419	0.003096	0.004342	0.006325	0.341787	
1781	AF054589	0.003096	0.004342	0.030568	-0.50762	
1782	H98552	0.003096	0.004342	0.017185	-0.1057	
1783	AI056697	0.003096	0.004342	0.000329	-0.20147	
1784	X00351	0.003096	0.005207	0.001506	-0.12928	ACTB
1785	AF006082	0.003096	0.005207	0.002797	-0.34587	ACTR2
1786	Y09443	0.003096	0.005207	0.002286	-0.17646	AGPS
1787	U22961	0.003096	0.005207	0.003092	0.147932	ALB
1788	AF002163	0.003096	0.005207	0.002447	-0.37588	AP3D1
1789	D87461	0.003096	0.005207	0.004809	-0.26338	BCL2L2
1790	AF013759	0.003096	0.005207	0.004946	-0.18574	CALU
1791	L22005	0.003096	0.005207	0.006442	0.131869	CDC34
1792	AL109689	0.003096	0.005207	0.013291	-0.24945	CGI-142
1793	U91543	0.003096	0.005207	0.014143	-0.25258	CHD3
1794	X82153	0.003096	0.005207	0.013882	-0.31742	CTSK
1795	AJ001687	0.003096	0.005207	0.000224	-0.64837	D12S2489E
1796	M13149	0.003096	0.005207	0.008717	-0.13824	HRG
1797	Y10313	0.003096	0.005207	0.006846	0.464769	IFRD1
1798	D63485	0.003096	0.005207	0.000985	-0.31599	IKKE
1799	D87077	0.003096	0.005207	0.043072	-0.21138	KIAA0240

1800	AB007864	0.003096	0.005207	0.001569	0.256672	KIAA0404
1801	X75346	0.003096	0.005207	0.001841	0.331699	MAPKAPK2
1802	L07648	0.003096	0.005207	0.010594	0.226817	MXI1
1803	AB028993	0.003096	0.005207	0.0247	0.133216	NLGN1
1804	D45333	0.003096	0.005207	0.002104	0.302454	PFDN1
1805	M65254	0.003096	0.005207	0.002619	0.262897	PPP2R1B
1806	M86852	0.003096	0.005207	0.004274	0.172251	PXMP3
1807	X97795	0.003096	0.005207	0.021131	-0.18349	RAD54L
1808	U14970	0.003096	0.005207	0.001894	-0.1353	RPS5
1809	X74570	0.003096	0.005207	0.00345	0.210049	SIAT4C
1810	X98248	0.003096	0.005207	0.010403	-0.50617	SORT1
1811	U17714	0.003096	0.005207	0.002081	-0.19372	ST13
1812	W28869	0.003096	0.005207	0.001369	-0.38498	TEGT
1813	M12125	0.003096	0.005207	0.000178	-0.09929	TPM2
1814	L27071	0.003096	0.005207	0.003834	-0.36074	TXK
1815	M60614	0.003096	0.005207	0.001757	-0.25283	WIT-1
1816	HG4074-HT4344	0.003096	0.005207	0.004175	0.589048	
1817	AL031846	0.003096	0.005207	0.004012	-0.42132	
1818	HG1980-HT2023	0.003096	0.005207	0.002314	0.711234	
1819	AF022853	0.047678	0.006683	0.002056	-0.30792	ABCC1
1820	X02994	0.047678	0.006683	0.036598	-0.12393	ADA
1821	D25304	0.047678	0.006683	0.002258	-0.44746	ARHGEF6
1822	M23115	0.047678	0.006683	0.016518	-0.1243	ATP2A2
1823	U87408	0.047678	0.006683	0.008628	-0.33961	B1
1824	AA135683	0.047678	0.006683	0.010045	0.6329	BASP1
1825	M22491	0.047678	0.006683	0.020141	-0.10386	BMP3
1826	M28170	0.047678	0.006683	0.014303	0.280093	CD19
1827	M16336	0.047678	0.006683	0.011755	-0.19993	CD2
1828	U37022	0.047678	0.006683	0.028135	-0.06885	CDK4
1829	U66469	0.047678	0.006683	0.004123	0.616896	CGR19
1830	AI037867	0.047678	0.006683	0.009634	-0.11973	CKTSF1B1
1831	J03071	0.047678	0.006683	0.011153	-0.23776	CSH2
1832	M55265	0.047678	0.006683	0.01278	-0.1479	CSNK2A1
1833	M33317	0.047678	0.006683	0.014832	-0.17753	CYP2A7
1834	U37143	0.013622	0.006683	0.001908	0.171138	CYP2J2
1835	AL049942	0.013622	0.006683	0.00076	-0.20245	DKFZP564F1422
1836	AL050015	0.013622	0.006683	0.008524	-0.13959	DKFZP564O243
1837	L35594	0.013622	0.006683	0.002806	0.216985	ENPP2
1838	J03796	0.047678	0.006683	0.002596	-0.28198	EPB41
1839	AC002398	0.013622	0.006683	0.003226	-0.27062	F25965
1840	X15376	0.013622	0.006683	0.014388	-0.15607	GABRG2
1841	M90656	0.047678	0.006683	0.006961	-0.15968	GCLC
1842	AF062006	0.013622	0.006683	0.001442	0.200117	GPR49
1843	X61755	0.013622	0.006683	0.000491	-0.19331	HOXC5
1844	D21851	0.047678	0.006683	0.017915	0.153927	KIAA0028

1845	AB007976	0.047678	0.006683	0.032427	0.228873	KIAA0507
1846	AI871396	0.047678	0.006683	0.001957	-0.48312	KIAA0557
1847	AB020660	0.047678	0.006683	0.001858	-0.27616	KIAA0853
1848	X93595	0.047678	0.006683	0.026214	0.245064	KIR3DL2
1849	AB002405	0.047678	0.006683	0.003681	-0.19481	LAK-4P
1850	X07228	0.047678	0.006683	0.046458	0.113484	LIPC
1851	U50529	0.047678	0.006683	0.001977	0.310499	LOC88523
1852	AF040963	0.047678	0.006683	0.012629	0.148739	MAD4
1853	U59423	0.047678	0.006683	0.01126	-0.1341	MADH1
1854	U85430	0.013622	0.006683	0.000224	-0.41454	NFATC3
1855	X80878	0.047678	0.006683	0.010021	-0.16096	NFRKB
1856	AF005043	0.013622	0.006683	0.00078	-0.15296	PARG
1857	D49818	0.047678	0.006683	0.021976	-0.10631	PFKFB4
1858	M28393	0.013622	0.006683	0.003241	-0.16419	PRF1
1859	Y00062	0.047678	0.006683	0.011868	-0.2415	PTPRC
1860	L07758	0.047678	0.006683	0.008943	0.201883	PWP1
1861	U57094	0.047678	0.006683	0.014944	-0.31108	RAB27A
1862	M35416	0.013622	0.006683	0.002789	-0.41233	RALB
1863	X75042	0.047678	0.006683	0.003614	0.659166	REL
1864	AF038250	0.047678	0.006683	0.004198	0.395171	SFRS3
1865	L27213	0.013622	0.006683	0.001014	-0.13065	SLC4A3
1866	Y09568	0.047678	0.006683	0.005799	-0.3407	SNAP23
1867	AA205857	0.013622	0.006683	0.00048	0.27495	SNRPD3
1868	U07794	0.047678	0.006683	0.007632	-0.20733	TXK
1869	J05428	0.013622	0.006683	0.00573	-0.08342	UGT2B7
1870	U09848	0.047678	0.006683	0.011538	-0.26846	ZNF36
1871	J00287	0.047678	0.006683	0.000953	-0.28381	
1872	AB007882	0.013622	0.009369	0.006034	-0.17275	ADCY6
1873	AF072810	0.013622	0.009369	0.016137	-0.32509	BAZ1B
1874	AB004066	0.013622	0.009369	0.00789	0.494455	BHLHB2
1875	U37547	0.013622	0.009369	0.00478	0.544595	BIRC2
1876	AB024704	0.013622	0.009369	0.010893	-0.11914	C20orf1
1877	AC004084	0.013622	0.009369	0.005491	-0.17437	CAPRI
1878	L12691	0.013622	0.009369	0.018291	-0.18848	DEFA3
1879	L19161	0.013622	0.009369	0.001645	-0.27253	EIF2S3
1880	M82882	0.013622	0.009369	0.003966	0.478256	ELF1
1881	X81625	0.013622	0.009369	0.003918	0.762544	ETF1
1882	M15059	0.013622	0.009369	0.035106	0.313247	FCER2
1883	AA284298	0.013622	0.009369	0.028745	-0.12535	FLJ22269
1884	U13044	0.013622	0.009369	0.017986	-0.32813	GABPA
1885	Z12173	0.013622	0.009369	0.001297	-0.32703	GNS
1886	U06631	0.013622	0.009369	0.003506	-0.37935	H326
1887	X75315	0.013622	0.009369	0.002959	1.06191	HSRNASEB
1888	AF064084	0.013622	0.009369	0.017927	-0.10308	ICMT
1889	AB002330	0.013622	0.009369	0.048512	-0.09076	KIAA0332
1890	AB014569	0.013622	0.009369	0.010011	0.709572	KIAA0669

1891	AI970189	0.013622	0.009369	0.001778	0.569801	KIAA0997
1892	AB028960	0.013622	0.009369	0.001825	-0.15403	KIAA1037
1893	AJ005273	0.013622	0.009369	0.001449	0.379277	KIN
1894	L00352	0.013622	0.009369	0.004231	0.554465	LDLR
1895	X54304	0.013622	0.009369	0.000863	-0.19567	MLCB
1896	AI693193	0.013622	0.009369	0.023978	-0.25831	MTX1
1897	AF047487	0.013622	0.009369	0.001312	-0.33746	NCK2
1898	AF037448	0.013622	0.009369	0.00743	0.204106	NSAP1
1899	AF000152	0.013622	0.009369	0.025216	-0.34592	OS4
1900	U02882	0.013622	0.009369	0.017536	0.892321	PDE4D
1901	X89416	0.013622	0.009369	0.005129	-0.1405	PPP5C
1902	U27516	0.013622	0.009369	0.004164	-0.17553	RAD52
1903	D23660	0.013622	0.009369	0.01215	0.149327	RPL4
1904	AB016247	0.013622	0.009369	0.019879	0.416634	SC5DL
1905	U44754	0.013622	0.009369	0.005273	0.158396	SNAPC1
1906	AI660929	0.013622	0.009369	0.000698	-0.15764	T1A-2
1907	X01060	0.013622	0.009369	0.005079	0.27369	TFRC
1908	J02973	0.013622	0.009369	0.006825	0.835338	THBD
1909	L41690	0.013622	0.009369	0.020209	-0.32814	TRADD
1910	X89066	0.013622	0.009369	0.000396	-0.2226	TRPC1
1911	AB024327	0.013622	0.009369	0.031	0.260875	UNRIP
1912	AF033199	0.013622	0.009369	0.02842	-0.1806	ZNF204
1913	AL080123	0.013622	0.009369	0.018447	0.215445	ZNF23
1914	AB007885	0.013622	0.009369	0.025803	-0.22701	ZNF262
1915	U40462	0.013622	0.009369	0.004101	-0.29722	ZNFN1A1
1916	HG3477-HT3670	0.013622	0.009369	0.00042	-0.2367	
1917	L42324	0.013622	0.009369	0.015195	0.283048	GPR18
1918	AA975427	0.013622	0.009369	0.002377	-0.26992	
1919	AL049957	0.013622	0.009369	0.007809	0.133451	
1920	AL022398	0.013622	0.009369	0.017529	-0.48579	
1921	HG2689-HT2785	0.013622	0.009369	0.029818	0.202486	
1922	AF034373	0.013622	0.014679	0.00591	-0.26511	A2LP
1923	X83467	0.013622	0.014679	0.006111	-0.25837	ABCD3
1924	U41766	0.047678	0.014679	0.014363	0.473526	ADAM9
1925	D67031	0.013622	0.014679	0.007826	-0.4645	ADD3
1926	U84011	0.013622	0.014679	0.012995	-0.2499	AGL
1927	M74088	0.013622	0.014679	0.038601	-0.16952	APC
1928	U67092	0.047678	0.014679	0.047381	-0.10935	ATM
1929	AI033692	0.047678	0.014679	0.010056	-0.2417	BCRP1
1930	X92106	0.013622	0.014679	0.001377	-0.33994	BLMH
1931	Z22535	0.047678	0.014679	0.021613	-0.09832	BMPR1A
1932	X79067	0.047678	0.014679	0.0381	0.14954	BRF1
1933	X86098	0.013622	0.014679	0.000807	-0.34829	BS69
1934	U72649	0.047678	0.014679	0.029157	0.227444	BTG2
1935	X95592	0.047678	0.014679	0.014127	0.201273	C1D

1936	D78586	0.047678	0.014679	0.028845	-0.05709	CAD
1937	D30742	0.047678	0.014679	0.028215	0.180381	CAMK4
1938	AF035582	0.047678	0.014679	0.002042	0.530946	CASK
1939	U60521	0.047678	0.014679	0.002353	0.552837	CASP9
1940	AL035079	0.013622	0.014679	0.00063	-0.78567	CAT
1941	AF094481	0.047678	0.014679	0.024569	0.149973	CGGBP1
1942	X83378	0.013622	0.014679	0.025603	0.133485	CLCN6
1943	AB002332	0.047678	0.014679	0.003136	-0.20009	CLOCK
1944	D13146	0.013622	0.014679	0.017967	-0.13385	CNP
1945	S80864	0.013622	0.014679	0.011106	-0.33164	CYCL
1946	D17530	0.047678	0.014679	0.005519	-0.15234	DBN1
1947	U87947	0.047678	0.014679	0.011279	0.222382	EMP3
1948	M60459	0.047678	0.014679	0.010174	-0.10156	EPOR
1949	AB018247	0.013622	0.014679	0.000348	0.423577	FE65L2
1950	AB028973	0.013622	0.014679	0.046458	-0.12088	FLJ10883
1951	AL080172	0.047678	0.014679	0.02693	-0.063	FLJ21919
1952	AF032886	0.047678	0.014679	0.009814	0.232307	FOXO3A
1953	U00928	0.047678	0.014679	0.01307	-0.0915	FUS
1954	M14660	0.047678	0.014679	0.011038	0.732462	FUT10
1955	AI935146	0.047678	0.014679	0.044653	0.246267	GALNT3
1956	U28811	0.047678	0.014679	0.007572	-0.21558	GLG1
1957	AF001903	0.013622	0.014679	0.001957	-0.28636	HADHSC
1958	Y09306	0.047678	0.014679	0.045083	-0.08024	HIPK3
1959	AL022723	0.047678	0.014679	0.041021	0.165267	HLA-G
1960	M80469	0.013622	0.014679	0.037453	-0.12099	HLA-J
1961	M16937	0.013622	0.014679	0.002262	-0.13536	HOXB7
1962	X98307	0.013622	0.014679	0.011852	-0.0908	HSHUR7SEQ
1963	HG2855-HT2995	0.047678	0.014679	0.030595	0.16813	HSP70
1964	X87949	0.047678	0.014679	0.028569	0.296273	HSPA5
1965	W68830	0.013622	0.014679	0.007971	-0.22855	HSPC022
1966	D49410	0.047678	0.014679	0.040369	0.153358	HUMIL3RA12
1967	AL049470	0.013622	0.014679	0.010492	0.283688	HYPB
1968	Y10659	0.047678	0.014679	0.024205	-0.1217	IL13RA1
1969	X52015	0.047678	0.014679	0.006637	0.417081	IL1RN
1970	AF047492	0.047678	0.014679	0.002557	0.25738	IMPG1
1971	U96919	0.013622	0.014679	0.003221	-0.19947	INPP4A
1972	U12897	0.013622	0.014679	0.002496	-0.15016	IPW
1973	S62539	0.013622	0.014679	0.012982	-0.20615	IRS1
1974	AF029778	0.047678	0.014679	0.018006	-0.14486	JAG2
1975	W25934	0.047678	0.014679	0.016925	0.363279	JTV1
1976	X56681	0.047678	0.014679	0.004935	0.713663	JUND
1977	M64934	0.047678	0.014679	0.003162	-0.1823	KEL
1978	D86975	0.047678	0.014679	0.048475	0.163408	KIAA0222
1979	AB020701	0.013622	0.014679	0.013946	0.283086	KIAA0894
1980	AB023141	0.047678	0.014679	0.017326	-0.33543	KIAA0924

1981	AB023148	0.013622	0.014679	0.016218	-0.27496	KIAA0931
1982	AB023227	0.047678	0.014679	0.043542	0.316063	KIAA1010
1983	AB028963	0.047678	0.014679	0.039194	-0.12296	KIAA1040
1984	AL080188	0.047678	0.014679	0.016745	-0.10387	KIAA1775
1985	AJ224162	0.013622	0.014679	0.002225	-0.24337	LAS
1986	L25931	0.013622	0.014679	0.00482	-0.2367	LBR
1987	AC004410	0.047678	0.014679	0.017457	0.210096	LOC56928
1988	AB009462	0.047678	0.014679	0.012892	0.131673	LRP3
1989	AF077820	0.013622	0.014679	0.003095	-0.40005	LRP5
1990	X59408	0.047678	0.014679	0.018321	-0.3029	MCP
1991	L13773	0.013622	0.014679	0.002741	-0.18297	MLLT2
1992	X82209	0.047678	0.014679	0.010828	0.178564	MN1
1993	X96401	0.013622	0.014679	0.001643	0.317165	MNT
1994	M30818	0.047678	0.014679	0.032832	0.292682	MX2
1995	V00568	0.013622	0.014679	0.008535	-0.58978	MYC
1996	D50692	0.013622	0.014679	0.043374	-0.20783	MYCBP
1997	AB007191	0.013622	0.014679	0.022026	-0.18098	MYCBP
1998	X17576	0.013622	0.014679	0.001641	-0.26027	NCK1
1999	X61498	0.013622	0.014679	0.006234	0.307667	NFKB2
2000	AF052093	0.047678	0.014679	0.001318	-0.31976	NJMU-R1
2001	X00737	0.047678	0.014679	0.037385	0.219194	NP
2002	U02020	0.047678	0.014679	0.014866	0.650286	PBEF
2003	X66362	0.047678	0.014679	0.006159	0.137944	PCTK3
2004	AF026086	0.047678	0.014679	0.006555	-0.18222	PEX1
2005	L25441	0.047678	0.014679	0.011907	0.146471	PGGT1B
2006	AL021366	0.013622	0.014679	0.002775	0.425217	PHF1
2007	D85418	0.013622	0.014679	0.004449	-0.31688	PIGC
2008	D30037	0.047678	0.014679	0.001579	-0.21226	PITPNB
2009	AB006746	0.047678	0.014679	0.0356	0.189986	PLSCR1
2010	AF054182	0.013622	0.014679	0.002098	-0.54761	PMPCB
2011	S87759	0.013622	0.014679	0.007522	0.39052	PPM1A
2012	M13057	0.047678	0.014679	0.032523	-0.19317	PRH1
2013	M64992	0.047678	0.014679	0.047326	0.178696	PSMA1
2014	X58288	0.047678	0.014679	0.002633	0.409542	PTPRM
2015	AD000092	0.047678	0.014679	0.028359	0.137917	RAD23A
2016	U79716	0.013622	0.014679	0.003409	0.195389	RELN
2017	U69198	0.047678	0.014679	0.048001	0.085316	RFNG
2018	AF117829	0.047678	0.014679	0.003668	0.377251	RIPK2
2019	AF039029	0.047678	0.014679	0.002146	-0.28622	RNUT1
2020	AW02154 2	0.013622	0.014679	0.000677	-0.29232	SAP18
2021	U64197	0.047678	0.014679	0.021124	0.220476	SCYA20
2022	AB023136	0.013622	0.014679	0.00288	-0.10963	SEC15B
2023	AF055006	0.013622	0.014679	0.011241	0.238955	SEC6
2024	Z46606	0.047678	0.014679	0.005778	-0.1566	SMARCA3
2025	L25270	0.047678	0.014679	0.002401	-0.15644	SMCX

2026	M60618	0.013622	0.014679	0.006316	0.235838	SP100
2027	AI739308	0.013622	0.014679	0.001861	-0.57419	SRP46
2028	U52960	0.047678	0.014679	0.02599	0.429086	SURB7
2029	D50863	0.013622	0.014679	0.006582	-0.13005	TESK1
2030	D64015	0.013622	0.014679	0.007587	-0.3629	TIAL1
2031	AB001523	0.047678	0.014679	0.027565	0.164838	TMEM1
2032	L21715	0.013622	0.014679	0.000862	0.309808	TNNI2
2033	AF045583	0.047678	0.014679	0.043887	-0.16757	TULP3
2034	AJ001340	0.013622	0.014679	0.002396	-0.17031	U3-55K
2035	AB015344	0.013622	0.014679	0.008107	-0.31161	UBQLN2
2036	J03824	0.013622	0.014679	0.005864	-0.18849	UROS
2037	AF022789	0.047678	0.014679	0.006582	0.309267	USP12
2038	U48801	0.013622	0.014679	0.003849	-0.17743	VEGFB
2039	HG544-HT544	0.047678	0.014679	0.010549	0.454218	
2040	S66666	0.013622	0.014679	0.003364	-0.14303	
2041	AI687419	0.047678	0.014679	0.039394	-0.3657	
2042	W28800	0.047678	0.014679	0.004582	0.270831	
2043	AL080111	0.013622	0.014679	0.001378	-0.36029	
2044	AF070536	0.047678	0.014679	0.006685	0.199364	
2045	AF070633	0.047678	0.014679	0.010142	-0.1635	
2046	AF054998	0.013622	0.014679	0.007913	-0.21157	
2047	HG3725-HT3981	0.047678	0.014679	0.027792	-0.11953	
2048	HG1614-HT1614	0.013622	0.014679	0.006999	-0.45233	
2049	M22324	0.013622	0.01669	0.009982	0.283293	ANPEP
2050	AC005955	0.013622	0.01669	0.004346	0.137324	CEACAM4
2051	S68134	0.013622	0.01669	0.005372	1.92718	CREM
2052	S68271	0.013622	0.01669	0.009154	1.49785	CREM
2053	M24069	0.013622	0.01669	0.003022	0.249971	CSDA
2054	AF000984	0.013622	0.01669	0.004295	0.46432	DBY
2055	AF055917	0.013622	0.01669	0.015434	0.102855	F2RL3
2056	U27333	0.013622	0.01669	0.012662	0.136047	FUT6
2057	X89887	0.013622	0.01669	0.009728	0.152829	HIRA
2058	L42243	0.013622	0.01669	0.002638	0.218644	IFNAR2
2059	AI950382	0.013622	0.01669	0.00744	0.601631	KIAA0585
2060	AI950382	0.013622	0.01669	0.002126	0.519735	KIAA0585
2061	U17760	0.013622	0.01669	0.044392	0.431131	LAMB3
2062	L48692	0.013622	0.01669	0.041233	0.63409	LOC56902
2063	X94232	0.013622	0.01669	0.016402	0.326694	MAPRE2
2064	AA037278	0.013622	0.01669	0.01607	0.119411	MGC10882
2065	L13740	0.013622	0.01669	0.007795	0.355688	NR4A1
2066	U12767	0.013622	0.01669	0.011648	1.30268	NR4A3
2067	D78579	0.013622	0.01669	0.005896	1.11766	NR4A3
2068	X17042	0.013622	0.01669	0.015594	0.239796	PRG1
2069	U48296	0.013622	0.01669	0.003124	0.864101	PTP4A1

2070	M83221	0.013622	0.01669	0.012321	0.192956	RELB
2071	AF107463	0.013622	0.01669	0.009662	0.419254	SPF30
2072	L47276	0.013622	0.01669	0.004673	0.194449	TOP2A
2073	X00734	0.013622	0.01669	0.010039	0.347307	TUBB5
2074	X51521	0.013622	0.01669	0.010303	0.60161	VIL2
2075	S54641	0.013622	0.01669	0.008483	0.183207	ZNF124
2076	M91029	0.013622	0.022759	0.010686	0.450612	AMPD2
2077	AB021638	0.136189	0.022759	0.024881	-0.1126	APBA3
2078	AL120559	0.013622	0.022759	0.004505	0.577915	ARPP-19
2079	AF039656	0.013622	0.022759	0.006991	0.68481	BASP1
2080	AB020623	0.047678	0.022759	0.009696	0.418826	BCAS2
2081	X60201	0.013622	0.022759	0.011758	-0.1576	BDNF
2082	U56637	0.047678	0.022759	0.008899	-0.28102	CAPZA1
2083	AW043690	0.047678	0.022759	0.031971	0.134862	CCK
2084	D13627	0.047678	0.022759	0.019298	0.203913	CCT8
2085	U56998	0.013622	0.022759	0.024403	0.442545	CNK
2086	U71267	0.047678	0.022759	0.007233	-0.13426	CNOT4
2087	F27891	0.047678	0.022759	0.02847	0.119514	COX6A2
2088	U78524	0.013622	0.022759	0.002554	0.353034	DDXBP1
2089	AF043733	0.047678	0.022759	0.005645	0.22771	DEDD
2090	X64229	0.013622	0.022759	0.013033	-0.20244	DEK
2091	AL050284	0.047678	0.022759	0.002819	0.232244	DKFZP586M1019
2092	L05147	0.013622	0.022759	0.021168	0.111752	DUSP3
2093	U15642	0.013622	0.022759	0.013339	0.474421	E2F5
2094	U31556	0.047678	0.022759	0.011303	0.335871	E2F5
2095	AC004262	0.047678	0.022759	0.004968	-0.25642	EMR2
2096	AA181196	0.047678	0.022759	0.009459	-0.10534	FLJ11712
2097	U74612	0.013622	0.022759	0.014802	-0.18783	FOXM1
2098	W28281	0.013622	0.022759	0.011042	0.813742	GABARAPL1
2099	AI183417	0.013622	0.022759	0.011016	0.117979	GABPB1
2100	L13720	0.013622	0.022759	0.014471	-0.1601	GAS6
2101	X15722	0.013622	0.022759	0.029451	-0.19175	GSR
2102	Y07595	0.013622	0.022759	0.003113	-0.20996	GTF2H4
2103	L43821	0.047678	0.022759	0.005863	-0.20401	HEF1
2104	L10379	0.013622	0.022759	0.02006	-0.15961	HRIHFB2206
2105	X99209	0.013622	0.022759	0.021333	-0.14942	HRMT1L1
2106	X77956	0.013622	0.022759	0.009598	0.591031	ID1
2107	AL021707	0.013622	0.022759	0.004161	1.79061	KIAA0063
2108	AB007896	0.013622	0.022759	0.006273	-0.41247	KIAA0436
2109	AB014528	0.047678	0.022759	0.001992	-0.31837	KIAA0628
2110	AB014607	0.013622	0.022759	0.000764	-0.15753	KIAA0707
2111	AB018290	0.013622	0.022759	0.034506	-0.28703	KIAA0747
2112	AB018337	0.013622	0.022759	0.008466	-0.41118	KIAA0794
2113	AB023161	0.013622	0.022759	0.018461	-0.15095	KIAA0944
2114	AB023202	0.013622	0.022759	0.005879	-0.19156	KIAA0985

2115	U80743	0.013622	0.022759	0.000544	-0.30322	KIAA1498
2116	X13794	0.047678	0.022759	0.018671	-0.12764	LDHB
2117	Z34975	0.013622	0.022759	0.012256	-0.29089	LDLC
2118	AI341656	0.047678	0.022759	0.021482	-0.26002	LIM
2119	X87342	0.013622	0.022759	0.006652	-0.23382	LLGL2
2120	U29671	0.047678	0.022759	0.001133	-0.2617	MAP3K1
2121	Z14138	0.013622	0.022759	0.00408	0.81232	MAP3K8
2122	AI743606	0.013622	0.022759	0.00269	-0.19764	MEL
2123	AF052183	0.013622	0.022759	0.002151	-0.19631	MGC2722
2124	AL050356	0.013622	0.022759	0.002743	-0.42417	MINPP1
2125	AF041081	0.013622	0.022759	0.019282	-0.21627	MN7
2126	U59302	0.013622	0.022759	0.003859	0.280175	NCOA1
2127	W28360	0.013622	0.022759	0.016633	0.272057	NCUBE1
2128	U97198	0.013622	0.022759	0.001352	-0.20163	NLP_1
2129	AA194159	0.013622	0.022759	0.004614	-0.40044	PEX10
2130	U38964	0.013622	0.022759	0.004912	-0.23793	PMS2L8
2131	D38498	0.013622	0.022759	0.003965	-0.58306	PMS2L9
2132	AA996066	0.013622	0.022759	0.003514	-0.21994	PMS2L9
2133	AB029028	0.013622	0.022759	0.027753	-0.29778	RAP140
2134	AA402524	0.047678	0.022759	0.005359	-0.11564	RBM9
2135	U79745	0.013622	0.022759	0.00409	0.777629	SLC16A6
2136	X98332	0.013622	0.022759	0.002282	-0.20078	SLC22A1
2137	D42045	0.013622	0.022759	0.006867	-0.19726	SNM1
2138	M76231	0.013622	0.022759	0.009942	0.13899	SPR
2139	U76366	0.013622	0.022759	0.015416	-0.09378	TCOF1
2140	U09087	0.013622	0.022759	0.00607	-0.26017	TMPO
2141	AF049140	0.047678	0.022759	0.011115	-0.21894	UBE2V2
2142	AF038962	0.047678	0.022759	0.007219	-0.44337	VDAC3
2143	D84145	0.013622	0.022759	0.002923	0.574155	WS-3
2144	Y09723	0.047678	0.022759	0.001292	0.234149	ZNF151
2145	AL049991	0.013622	0.022759	0.007094	0.245237	
2146	AL050148	0.013622	0.022759	0.013128	-0.26398	
2147	AI014538	0.013622	0.022759	0.003507	-0.15278	
2148	AI732885	0.047678	0.022759	0.043886	-0.10293	
2149	U14573	0.013622	0.022759	0.04259	-0.11614	
2150	U82987	0.013622	0.024606	0.00343	-0.17272	BBC3
2151	L12168	0.013622	0.024606	0.007944	-0.22028	CAP
2152	V00571	0.013622	0.024606	0.005873	0.132015	CRH
2153	AL022398	0.013622	0.024606	0.015005	-0.44535	DJ434O14.3
2154	AL080081	0.013622	0.024606	0.007659	0.548836	DNAJB9
2155	X85116	0.013622	0.024606	0.039531	-0.24601	EPB72
2156	AJ007669	0.013622	0.024606	0.019404	-0.23162	FANCG
2157	AW024285	0.013622	0.024606	0.007049	0.311562	FLJ12443
2158	W27666	0.013622	0.024606	0.009544	-0.25685	FLJ14393
2159	AA908993	0.013622	0.024606	0.015356	-0.12684	FLJ14393

2160	U90917	0.013622	0.024606	0.016602	-0.23386	FOXM1
2161	AF017445	0.013622	0.024606	0.025525	-0.33517	FPGT
2162	AJ238764	0.013622	0.024606	0.030667	0.197763	GNE
2163	J04501	0.013622	0.024606	0.007821	-0.23523	GYS1
2164	X56841	0.013622	0.024606	0.022605	-0.23469	HLA-E
2165	M63438	0.013622	0.024606	0.005389	-0.75873	IGKC
2166	S66213	0.013622	0.024606	0.011362	-0.09802	ITGA6
2167	AB007870	0.013622	0.024606	0.002855	0.657213	KIAA0410
2168	N29665	0.013622	0.024606	0.008301	-0.49779	KIAA0618
2169	AB018353	0.013622	0.024606	0.033864	-0.3542	KIAA0810
2170	D10522	0.013622	0.024606	0.028464	0.22227	MACS
2171	AF004709	0.013622	0.024606	0.018118	-0.09931	MAPK13
2172	W28275	0.013622	0.024606	0.005871	-0.27591	MGC11061
2173	AF087020	0.013622	0.024606	0.032064	-0.13544	MPZL1
2174	U61981	0.013622	0.024606	0.012069	-0.20932	MSH3
2175	U90942	0.013622	0.024606	0.004002	0.179029	MYO5A
2176	D50370	0.013622	0.024606	0.008327	-0.11492	NAP1L3
2177	U91512	0.013622	0.024606	0.00493	0.549889	NINJ1
2178	AF069987	0.013622	0.024606	0.007336	-0.16953	NIT1
2179	U37689	0.013622	0.024606	0.007097	-0.17369	POLR2H
2180	L19067	0.013622	0.024606	0.006406	0.148517	RELA
2181	X13482	0.013622	0.024606	0.016873	0.241998	SNRPA1
2182	D16827	0.013622	0.024606	0.004314	-0.16954	SSTR5
2183	AB011420	0.013622	0.024606	0.030791	0.171669	STK17A
2184	L39060	0.013622	0.024606	0.026797	-0.24028	TAF1A
2185	AB011169	0.013622	0.024606	0.004017	-0.24355	TEB4
2186	U69108	0.013622	0.024606	0.024472	-0.17595	TRAF5
2187	AB011004	0.013622	0.024606	0.00265	1.03158	UAP1
2188	AB014584	0.013622	0.024606	0.028525	-0.1337	UBE4B
2189	HG3914-HT4184	0.013622	0.024606	0.025854	-0.12454	
2190	Z32860	0.013622	0.024606	0.002037	-0.11041	
2191	U25849	0.013622	0.024606	0.00632	-0.43498	
2192	AF052100	0.013622	0.024606	0.006718	-0.2297	
2193	X59268	0.013622	0.024606	0.003586	0.479423	GTF2B
2194	AF007142	0.013622	0.024606	0.01864	-0.34584	
2195	AI312646	0.013622	0.024606	0.027596	-0.14991	
2196	AL022318	0.047678	0.028192	0.049355	-0.11704	APOBEC1L
2197	M30704	0.047678	0.028192	0.00926	0.279668	AREG
2198	AF001307	0.047678	0.028192	0.018109	-0.12594	ARNT
2199	AB020680	0.047678	0.028192	0.007009	0.227256	BAG5
2200	AF018631	0.047678	0.028192	0.008344	-0.13689	BTD
2201	D64110	0.047678	0.028192	0.022809	0.398412	BTG3
2202	Z11697	0.047678	0.028192	0.024131	0.750492	CD83
2203	M31516	0.047678	0.028192	0.021562	0.517068	DAF
2204	AF000982	0.047678	0.028192	0.025357	0.29808	DDX3

2205	L77566	0.047678	0.028192	0.01243	0.178957	DGSI
2206	AL096725	0.047678	0.028192	0.007381	0.436688	DKFZP434B103
2207	AL080201	0.047678	0.028192	0.044829	-0.11576	DKFZP434F162
2208	AL050286	0.047678	0.028192	0.004267	-0.22397	DKFZP586A011
2209	Y13350	0.047678	0.028192	0.015562	0.137002	DNAJA2
2210	AJ223333	0.047678	0.028192	0.013836	-0.17437	DNMT2
2211	L34075	0.047678	0.028192	0.013848	-0.25236	FRAP1
2212	D31766	0.047678	0.028192	0.029287	-0.09623	GNPI
2213	Z80776	0.047678	0.028192	0.002034	0.143491	H2AFG
2214	K03183	0.047678	0.028192	0.040298	0.163306	HUMCGBBA3
2215	X57025	0.047678	0.028192	0.009135	0.437394	IGF1
2216	X56681	0.047678	0.028192	0.012885	0.423181	JUND
2217	AB007916	0.047678	0.028192	0.00772	-0.45744	KIAA0447
2218	AI672098	0.047678	0.028192	0.014331	0.160649	KIAA0934
2219	AB029020	0.047678	0.028192	0.035285	-0.3101	KIAA1097
2220	W27233	0.047678	0.028192	0.019918	-0.24802	KIDINS220
2221	AL049341	0.047678	0.028192	0.001943	-0.3086	LOC57209
2222	AL049422	0.047678	0.028192	0.028823	0.264129	LOC84549
2223	AF010193	0.047678	0.028192	0.003729	0.927225	MADH7
2224	AF007134	0.047678	0.028192	0.009151	-0.1209	MAPK8IP1
2225	L04731	0.047678	0.028192	0.025599	-0.07236	MLL
2226	AB014547	0.047678	0.028192	0.023787	-0.15831	MTMR4
2227	U91616	0.047678	0.028192	0.018681	0.377931	NFKBIE
2228	X75918	0.047678	0.028192	0.019713	1.21948	NR4A2
2229	AL049842	0.047678	0.028192	0.022698	0.201258	NUFIP1
2230	U57843	0.047678	0.028192	0.011796	-0.13969	PIK3CD
2231	S76965	0.047678	0.028192	0.012413	0.426208	PKIA
2232	AL023553	0.047678	0.028192	0.00321	-0.15608	PMM1
2233	M93425	0.047678	0.028192	0.019899	-0.36854	PTPN12
2234	AF044968	0.047678	0.028192	0.006887	0.121898	PVRL2
2235	M28211	0.047678	0.028192	0.050065	-0.08518	RAB4
2236	AF083255	0.047678	0.028192	0.021248	-0.27368	RNAHP
2237	U04897	0.047678	0.028192	0.013893	0.278167	RORA
2238	AL031228	0.047678	0.028192	0.020491	-0.22382	SACM2L
2239	Y08262	0.047678	0.028192	0.008184	-0.34195	SCA2
2240	AF000652	0.047678	0.028192	0.001533	0.415218	SDCBP
2241	D31891	0.047678	0.028192	0.00536	-0.18144	SETDB1
2242	X66079	0.047678	0.028192	0.008707	0.129642	SPIB
2243	Z96932	0.047678	0.028192	0.013622	-0.14003	SSNA1
2244	D43642	0.047678	0.028192	0.015302	-0.26409	TCFL1
2245	D50919	0.047678	0.028192	0.016207	-0.23972	TRIM14
2246	X01703	0.047678	0.028192	0.004339	0.386096	TUBA3
2247	AF022375	0.047678	0.028192	0.015198	0.503607	VEGF
2248	AF062346	0.047678	0.028192	0.014763	0.455053	ZNF216
2249	J04755	0.047678	0.028192	0.014444	0.302274	
2250	AA524802	0.047678	0.028192	0.036226	-0.24775	

2251	AL096749	0.047678	0.028192	0.017041	0.106309	
2252	M21259	0.047678	0.028192	0.025927	0.18378	
2253	X61587	0.047678	0.037364	0.024028	0.222788	ARHG
2254	J04027	0.047678	0.037364	0.019918	0.336927	ATP2B1
2255	W28091	0.047678	0.037364	0.016936	-0.1567	BBS4
2256	U03106	0.047678	0.037364	0.004064	0.915096	CDKN1A
2257	AL049924	0.047678	0.037364	0.001517	-0.23208	DKFZP547G1110
2258	L19161	0.047678	0.037364	0.006578	-0.49859	EIF2S3
2259	AF052123	0.136189	0.037364	0.013524	-0.24445	FLJ10814
2260	AA522530	0.047678	0.037364	0.038021	0.413536	FLJ20500
2261	AJ011001	0.047678	0.037364	0.016436	-0.63045	GPR56
2262	U50079	0.047678	0.037364	0.013178	-0.37546	HDAC1
2263	AI796944	0.047678	0.037364	0.011597	0.216392	HIS1
2264	S82986	0.047678	0.037364	0.006441	-0.20652	HOXC6
2265	AB011173	0.047678	0.037364	0.01376	-0.26283	KIAA0601
2266	AB023160	0.047678	0.037364	0.029467	-0.23276	KIAA0943
2267	AJ001685	0.047678	0.037364	0.015208	-0.48906	KLRC3
2268	AJ000673	0.047678	0.037364	0.009021	-0.38103	KLRD1
2269	AB002450	0.047678	0.037364	0.003391	-0.37426	LOC51014
2270	U68385	0.047678	0.037364	0.007651	-0.16327	MEIS3
2271	AI688516	0.047678	0.037364	0.017859	-0.15146	NDUFA2
2272	W28770	0.047678	0.037364	0.005269	-0.16121	NP25
2273	L41827	0.047678	0.037364	0.011308	0.139896	NRG1
2274	X84373	0.047678	0.037364	0.00725	0.77533	NRIP1
2275	M25897	0.047678	0.037364	0.025747	-0.41462	PF4
2276	U50062	0.047678	0.037364	0.018154	0.19401	RIPK1
2277	AJ011785	0.047678	0.037364	0.017907	-0.07616	SIX6
2278	X70683	0.047678	0.037364	0.0155	-0.10219	SOX4
2279	AL035699	0.047678	0.037364	0.006561	-0.15185	TBPL1
2280	D15050	0.047678	0.037364	0.016133	0.990791	TCF8
2281	AF017146	0.047678	0.037364	0.002975	-0.20652	TOP3B
2282	U54996	0.047678	0.037364	0.00691	-0.17359	ZW10
2283	HG4234-HT	0.047678	0.037364	0.003258	-0.13985	
2284	X04500	0.047678	0.058634	0.02228	0.857952	IL1B

Table IV: Differential Gene Expression in MOG-reactive T-cells- MS vs. Healthy

SEQ ID NO:	Identifier	Symbol	Name	Function	Fold	Pvalue
	Up regulated				**Change**	**t-test**
2285	M35878	IGFBP3	insulin-like growth factor binding protein 3	modulate IGF activity	5.8	0.03
2286	AB002318	KIAA0320	KIAA0320 protein		2.4	0.05
2287	AF024710	VEGF	vascular endothelial growth factor	endothelial cell proliferation	2.3	0.02

2288	AA628946	KHSRP	KH-type splicing regulatory protein	mRNA processing	2.2	0.01
2289	L42374	PPP2R5B	protein phosphatase 2, regulatory subunit B	protein phosphatase	2.1	0.05
2290	U54644	TUB	tubby (mouse) homolog	may be a transcription factor	1.8	0.01
2291	AB023167	KIAA0950	lifeguard	Apoptosis	1.8	0.006
2292	X62654	CD63	CD63 antigen (melanoma 1 antigen)	growth regulation	1.8	0.03
2293	H98552		cDNA DKFZp586I0523		1.8	0.01
2294	AL050395	MOF	member of MYST acetyl transferases	histone acetyl transferases	1.7	0.03
2295	L27213	SLC4A3	solute carrier family 4, anion exchange 3	inorganic anion exchanger	1.7	0.01
2296	AF014837	M6A	putative methyltransferase	Transcription factor	1.6	0.05
2297	AB014537	KIAA0637	KIAA0637 gene product	Apoptosis	1.5	0.003
2298	D13969	ZNF144	zinc finger protein 144 (Mel-18)	DNA-Binding protein	1.5	0.04
2299	AJ012590	H6PD	hexose-6-phosphate dehydrogenase	Oxidoreductase	1.5	0.04
2300	M13995	BCL2	B-cell CLL/lymphoma 2	Apoptosis	1.5	0.03
2301	AI760801		chromosome 19, cosmid R31180		1.5	0.009
2302	AI660963	MAP3K12	mitogen-activated protein 3 kinase 12	Transferase cytoplasmic	1.5	0.02
2303	**Down regulated** D45248	PSME2	proteasome activator subunit 2 (PA28 beta)	Protein degradation	-1.5	0.04
2304	W28612		ESTs		-1.5	0.02
2305	Z46389	VASP	vasodilator-stimulated phosphoprotein	Signal transduction	-1.6	0.02
2306	AA152202	FLJ14639	hypothetical protein FLJ14639		-1.6	0.02
2307	AF080561	RBM14	RNA binding motif protein 14	RNA binding protein	-1.7	0.03
2308	D50922	KIAA0132	Kelch-like ECH-associated protein 1	ECH-associated protein 1	-1.7	0.03
2309	AF025441	OIP5	Opa-interacting protein 5		-1.8	0.04
2310	AF080227	EED	embryonic ectoderm development	transcriptional repressor	-1.8	0.04
2311	D87957	RQCD1	required for cell differentiation	sex differentiation	-1.9	0.03
2312	X61498	NFKB2	nuclear factor of kappa light polypeptide Bcells	expression of inflammatory genes	-1.9	0.05
2313	X52425	IL4R	interleukin 4 receptor	receptor signalling protein	-2	0.04
2314	L08069	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	protein folding and transport	-2	0.04

2315	AF071504	STX11	syntaxin 11	protein transport	-2.1	0.03
2316	M11717	HSPA1A	heat shock 70kD protein 1A	heat shock response	-2.2	0.03
2317	M59830	HSPA1B	heat shock 70kD protein 1B	heat shock response	-2.2	0.03
2318	M16441	TNF	Human tumor necrosis factor	Inflammatory response	-2.3	0.05
2319	D89077	SLA	Src-like-adapter		-2.4	0.05
2320	U77949	CDC6	cell division cycle 6, S. cerevisiae homolog	DNA replication checkpoint	-2.5	0.02
2321	D38549	KIAA0068	KIAA0068 protein		-2.5	0.01
2322	L23959	TFDP1	transcription factor Dp-1	cycle progression G1 to S-phase	-2.5	0.01
2323	L78833	BRCA1	Breast cancer susceptibility gene		-2.7	0.04
2324	M63193	ECGF1	endothelial cell growth factor 1	stimulates angiogenesis	-2.8	0.01
2325	AF035625	STK11	serine/threonine kinase 11	Peutz-Jeghers syndrome	-2.9	0.04
2326	J04130	SCYA4	small inducible cytokine A4	Cell-to-cell signalling	-2.9	0.05
2327	X93086	BLVRA	biliverdin reductase A	biliverdin reductase	-4	0.03

Table V: Differential Gene Expression in Probable MS vs. Healthy

SEQ ID NO:	Identification	TNOM PValue	Info PValue	t-Test PValue	Log Fold Change	Gene Symbol
2328	NM_018049.1	0.000233	0.000233	2.46E-05	0.438337	FLJ10297
2329	NM_005886.1	0.000233	0.000233	0.000553	0.35972	KATNB1
2330	NM_000161.1	0.000233	0.000233	0.000297	-0.48848	GCH1
2331	NM_001539.1	0.000233	0.000233	0.000144	-0.58017	DNAJA1
2332	AF349571.1	0.004202	0.004202	0.000274	1.78925	HBA1
2333	M25079.1	0.004202	0.004202	0.000247	1.59503	HBB
2334	V00489	0.004202	0.004202	0.000268	1.54947	
2335	BC005931.1	0.004202	0.004202	0.000296	1.48707	HBA2
2336	T50399	0.004202	0.004202	0.000275	1.43533	HBA2
2337	NM_024567.1	0.004202	0.004202	0.002206	1.42146	FLJ21616
2338	AF105974.1	0.004202	0.004202	0.001086	1.3896	HBA1
2339	NM_000558.2	0.004202	0.004202	0.000707	1.3348	HBA1
2340	AI133353	0.004202	0.004202	0.000897	1.29746	HBG2
2341	AF059180	0.004202	0.004202	0.000309	1.29355	
2342	AF349114.1	0.004202	0.004202	0.000163	1.27511	HBB
2343	BE547674	0.004202	0.004202	0.002947	0.636619	
2344	NM_012452.1	0.004202	0.004202	0.000541	0.570818	TNFRSF13B
2345	AA314406	0.004202	0.001401	0.002013	0.520631	TRAP95
2346	NM_015909.1	0.004202	0.001401	0.000398	0.501733	NAG

2347	NM_006868.1	0.004202	0.004202	0.002711	0.49862	RAB31
2348	BC000305.1	0.004202	0.004202	0.006921	0.475733	CASP6
2349	L77566	0.004202	0.001401	0.00033	0.446293	DGSI
2350	BF971416	0.004202	0.004202	0.002405	0.410742	DKFZP586N0721
2351	BE879367	0.004202	0.004202	0.00056	0.382484	AKAP2
2352	NM_001640.2	0.004202	0.001401	0.004091	0.36631	APEH
2353	BC001808.1	0.004202	0.004202	0.012997	0.347043	NM23-H6
2354	AL049539	0.004202	0.004202	0.010738	0.2822	KIAA0255
2355	BC000580.1	0.004202	0.001401	0.014166	0.270658	PH-4
2356	NM_012151.2	0.004202	0.001401	0.000685	0.267664	F8A
2357	BC004423.1	0.004202	0.004202	0.012194	0.249144	TNRC5
2358	NM_004890.1	0.004202	0.001401	0.010332	0.134439	SPAG7
2359	AB029040	0.004202	0.004202	0.010819	-0.14172	KIAA1117
2360	NM_025160.1	0.004202	0.001401	0.004986	-0.21141	FLJ21016
2361	AW162015	0.004202	0.004202	0.301224	-0.24766	ZNF143
2362	NM_005574.2	0.004202	0.004202	0.107595	-0.24939	LMO2
2363	NM_014670.1	0.004202	0.004202	0.025534	-0.27225	BZW1
2364	AL117643.1	0.004202	0.004202	0.046495	-0.27766	
2365	AA628948	0.004202	0.001401	0.000319	-0.28951	ADSS
2366	AF251062.1	0.004202	0.001401	0.000435	-0.30924	LOC84549
2367	AL564683	0.004202	0.004202	0.018258	-0.44633	CEBPB
2368	NM_014999.1	0.004202	0.004202	0.001021	-0.47304	RAB21
2369	NM_017723.1	0.004202	0.004202	0.02759	-0.49548	FLJ20245
2370	NM_003264.1	0.004202	0.004202	0.002592	-0.49551	TLR2
2371	AF062347.1	0.004202	0.004202	0.00529	-0.51432	ZNF216
2372	NM_004556.1	0.004202	0.004202	0.001134	-0.53489	NFKBIE
2373	U92014.1	0.004202	0.004202	0.003064	-0.59511	
2374	NM_014778.1	0.004202	0.004202	0.001106	-0.65156	KIAA0410
2375	NM_015384.1	0.004202	0.004202	0.002943	-0.68193	IDN3
2376	AK022513.1	0.004202	0.004202	0.001326	-0.68416	DUSP10
2377	NM_003246.1	0.004202	0.001401	0.000162	-1.44745	THBS1
2378	AI812030	0.004202	0.001401	7.42E-05	-1.51098	THBS1
2379	NM_000559.1	0.035714	0.035247	0.006202	1.93991	HBG1
2380	NM_000184.1	0.035714	0.04225	0.009164	1.67513	HBG2
2381	NM_005564.1	0.035714	0.04225	0.010814	1.03322	LCN2
2382	AF274863.1	0.035714	0.00747	0.007719	0.952868	SEC31B-1
2383	NM_002288.2	0.035714	0.015406	0.010689	0.834313	LAIR2
2384	M87789.1	0.035714	0.04225	0.058518	0.79032	IGHG3
2385	NM_005764.1	0.035714	0.04225	0.053679	0.789147	DD96
2386	AK000168.1	0.035714	0.04225	0.038176	0.763766	KIAA1919
2387	NM_020037.1	0.035714	0.035247	0.061379	0.746143	ABCC3
2388	AF103529.1	0.035714	0.035247	0.015284	0.736268	
2389	AV698647	0.035714	0.035247	0.017411	0.616137	IGLJ3
2390	AI357539	0.035714	0.04225	0.00558	0.601843	MGC4126
2391	NM_015935.1	0.035714	0.035247	0.021683	0.593818	CGI-01

2392	D38535	0.035714	0.04225	0.016025	0.571168	ITIH4
2393	AA723370	0.035714	0.04225	0.039917	0.570325	LOC51011
2394	AF227968.1	0.035714	0.00747	0.005308	0.566516	SH2B
2395	X12530.1	0.035714	0.04225	0.056335	0.559172	MS4A1
2396	AI348935	0.035714	0.035247	0.014129	0.546773	CALR
2397	NM_003422.1	0.035714	0.04225	0.006737	0.536815	ZNF42
2398	NM_015559.1	0.035714	0.04225	0.028795	0.536316	SETBP1
2399	NM_013378.1	0.035714	0.035247	0.005191	0.532564	VPREB3
2400	NM_004912.1	0.035714	0.015406	0.003037	0.52082	CCM1
2401	NM_006230.1	0.035714	0.015406	0.007471	0.517979	POLD2
2402	NM_006235.1	0.035714	0.035247	0.021726	0.515263	POU2AF1
2403	AL037557	0.035714	0.00747	0.002786	0.511724	POLR2I
2404	NM_014703.1	0.035714	0.00747	0.006709	0.4938	KIAA0800
2405	NM_015670.1	0.035714	0.035247	0.045708	0.464156	SENP3
2406	AA643304	0.035714	0.015406	0.004712	0.459694	
2407	AI948503	0.035714	0.04225	0.017964	0.45625	ABCC4
2408	BC002807.1	0.035714	0.04225	0.100759	0.455683	MS4A1
2409	AF123539.1	0.035714	0.035247	0.028286	0.454603	HTCD37
2410	AA149644	0.035714	0.00747	0.02413	0.450082	JAM3
2411	BC000585.1	0.035714	0.04225	0.033113	0.44368	SLC21A11
2412	AB044806.1	0.035714	0.04225	0.007766	0.433985	KCNH2
2413	U37025	0.035714	0.035247	0.046971	0.427213	SULT1A1
2414	NM_020166.2	0.035714	0.035247	0.006318	0.423798	MCCC1
2415	NM_002876.1	0.035714	0.035247	0.026644	0.414867	RAD51C
2416	NM_002387.1	0.035714	0.035247	0.01092	0.409481	MCC
2417	NM_005816.1	0.035714	0.04225	0.103051	0.407348	TACTILE
2418	H95263	0.035714	0.035247	0.069113	0.406766	
2419	NM_003146.1	0.035714	0.035247	0.003146	0.405309	SSRP1
2420	NM_003550.1	0.035714	0.035247	0.054105	0.403851	MAD1L1
2421	AK022494.1	0.035714	0.00747	0.001189	0.397073	RAB3GAP
2422	NM_006400.2	0.035714	0.035247	0.021072	0.396297	DCTN2
2423	NM_006012.1	0.035714	0.035247	0.015241	0.394779	CLPP
2424	NM_014921.1	0.035714	0.035247	0.014463	0.394308	LEC2
2425	NM_025056.1	0.035714	0.00747	0.01912	0.393739	FLJ23185
2426	NM_003573.1	0.035714	0.04225	0.026053	0.393337	LTBP4
2427	NM_000132.2	0.035714	0.035247	0.005292	0.392442	F8
2428	AF031824.1	0.035714	0.035247	0.190243	0.389129	CST7
2429	NM_001841.1	0.035714	0.035247	0.07115	0.387067	CNR2
2430	NM_018391.1	0.035714	0.035247	0.138584	0.386982	FLJ23277
2431	U79248.1	0.035714	0.00747	0.007475	0.386419	
2432	NM_024332.1	0.035714	0.04225	0.039154	0.386198	C6.1A
2433	BF510692	0.035714	0.04225	0.046782	0.385324	PAX5
2434	AA243774	0.035714	0.035247	0.050456	0.381631	MMP24
2435	AL121964	0.035714	0.035247	0.107681	0.373759	MAP3K7
2436	L25275.1	0.035714	0.035247	0.020684	0.372971	SULT1A3
2437	AB018289.1	0.035714	0.035247	0.002286	0.37263	KIAA0746

2438	NM_000294.1	0.035714	0.035247	0.011432	0.367693	PHKG2
2439	BC001906.1	0.035714	0.035247	0.107947	0.366899	MTX1
2440	NM_000651.1	0.035714	0.04225	0.047953	0.365471	CR1
2441	NM_001667.1	0.035714	0.00747	0.009661	0.362105	ARL2
2442	AI133727	0.035714	0.00747	0.018354	0.358884	ZAP
2443	BC002873.1	0.035714	0.035247	0.048711	0.358052	DKFZP564J0123
2444	NM_004178.2	0.035714	0.035247	0.007313	0.356459	TARBP2
2445	BG532929	0.035714	0.035247	0.037215	0.356254	SSB
2446	NM_018094.1	0.035714	0.035247	0.014302	0.351314	GSPT2
2447	AC004531	0.035714	0.00747	0.01714	0.350445	DDX28
2448	NM_001981.1	0.035714	0.035247	0.010776	0.347051	EPS15
2449	AB020689.1	0.035714	0.035247	0.024594	0.346253	KIAA0882
2450	NM_001055.1	0.035714	0.035247	0.056416	0.344937	SULT1A1
2451	NM_022067.1	0.035714	0.035247	0.001332	0.337713	FLJ12707
2452	NM_000195.1	0.035714	0.00747	0.014156	0.3312	HPS1
2453	NM_022914.1	0.035714	0.00747	0.167735	0.331082	24432
2454	NM_003627.1	0.035714	0.035247	0.062759	0.330371	POV1
2455	NM_022060.1	0.035714	0.035247	0.010717	0.328122	FLJ12816
2456	BF446180	0.035714	0.035247	0.02537	0.326347	PDCD2
2457	U28169.1	0.035714	0.035247	0.0891	0.326218	SULT1A2
2458	AF316873.1	0.035714	0.035247	0.022727	0.3257	PINK1
2459	NM_017615.1	0.035714	0.035247	0.087717	0.325056	FLJ20003
2460	NM_015853.1	0.035714	0.035247	0.021537	0.321089	LOC51035
2461	NM_018449.1	0.035714	0.035247	0.01461	0.318475	UBAP2
2462	NM_007056.1	0.035714	0.035247	0.013827	0.318086	SWAP2
2463	AV702994	0.035714	0.035247	0.010766	0.316138	LOC51668
2464	AK021884.1	0.035714	0.04225	0.016862	0.315879	NPEPPS
2465	U64898.1	0.035714	0.035247	0.012705	0.309446	NRD1
2466	AI431902	0.035714	0.035247	0.026163	0.307321	FLJ13491
2467	NM_003689.1	0.035714	0.04225	0.03366	0.306281	AKR7A2
2468	BE791629	0.035714	0.00747	0.039522	0.304821	CGTHBA
2469	NM_016194.1	0.035714	0.035247	0.060249	0.303474	GNB5
2470	NM_014965.1	0.035714	0.035247	0.013547	0.298042	KIAA1042
2471	NM_003363.1	0.035714	0.035247	0.018393	0.295239	USP4
2472	U88964	0.035714	0.035247	0.019349	0.294427	ISG20
2473	BC001782.1	0.035714	0.035247	0.059026	0.293156	GAS2L1
2474	BC004361.1	0.035714	0.04225	0.084538	0.292509	PSCD2
2475	NM_017840.1	0.035714	0.035247	0.003929	0.290472	MRPL16
2476	NM_006321.1	0.035714	0.015406	0.006688	0.288723	ARIH2
2477	AI341234	0.035714	0.035247	0.007356	0.284699	CORO1B
2478	N20923	0.035714	0.035247	0.020271	0.280552	FYN
2479	L42531.1	0.035714	0.035247	0.008554	0.280023	
2480	AK000818.1	0.035714	0.035247	0.02226	0.277695	FLJ20811
2481	NM_000633.1	0.035714	0.035247	0.044639	0.276897	BCL2
2482	BE551347	0.035714	0.035247	0.209003	0.276406	FLJ13052
2483	AK000161.1	0.035714	0.04225	0.016752	0.276103	FLJ20154

2484	AI798908	0.035714	0.04225	0.015969	0.274921	KIAA0226
2485	NM_005111.1	0.035714	0.035247	0.01405	0.273732	CRYZL1
2486	NM_024551.1	0.035714	0.035247	0.00372	0.272684	FLJ21432
2487	BC006214.1	0.035714	0.00747	0.006244	0.268704	IRO039700
2488	AI123527	0.035714	0.04225	0.105392	0.268349	KIAA0092
2489	NM_004379.1	0.035714	0.035247	0.047229	0.267796	CREB1
2490	AA643304	0.035714	0.035247	0.039678	0.258201	
2491	NM_013417.1	0.035714	0.035247	0.047087	0.257738	IARS
2492	AK025432.1	0.035714	0.035247	0.051871	0.257456	KIAA0564
2493	AB028960	0.035714	0.04225	0.040942	0.254827	KIAA1037
2494	NM_000048.1	0.035714	0.04225	0.038931	0.254447	ASL
2495	NM_002808.1	0.035714	0.035247	0.023966	0.250129	PSMD2
2496	NM_001054.1	0.035714	0.035247	0.062598	0.248696	SULT1A2
2497	NM_005428.2	0.035714	0.035247	0.007185	0.248439	VAV1
2498	NM_022758.1	0.035714	0.04225	0.011489	0.246401	FLJ22195
2499	AY009128.1	0.035714	0.035247	0.084938	0.246257	NIFU
2500	AB017004.1	0.035714	0.035247	0.079567	0.244954	PMS2L8
2501	NM_000249.1	0.035714	0.04225	0.021274	0.243441	MLH1
2502	U51007.1	0.035714	0.035247	0.042753	0.242223	
2503	BC002640.1	0.035714	0.035247	0.074751	0.240603	
2504	NM_016284.1	0.035714	0.00747	0.001929	0.240076	KIAA1007
2505	NM_002414.1	0.035714	0.035247	0.063998	0.239013	MIC2
2506	BC000212.1	0.035714	0.035247	0.021052	0.237577	GTF3C2
2507	NM_004398.2	0.035714	0.035247	0.040656	0.235252	DDX10
2508	NM_024713.1	0.035714	0.035247	0.048887	0.234927	FLJ22557
2509	NM_002810.1	0.035714	0.035247	0.038558	0.234593	PSMD4
2510	NM_030580.1	0.035714	0.035247	0.031263	0.233466	MGC10520
2511	AB007896.1	0.035714	0.035247	0.211816	0.231563	KIAA0436
2512	NM_003954.1	0.035714	0.04225	0.051916	0.230862	MAP3K14
2513	NM_025207.1	0.035714	0.035247	0.020823	0.230015	PP591
2514	NM_016323.1	0.035714	0.035247	0.051393	0.228764	LOC51191
2515	NM_016069.1	0.035714	0.04225	0.132766	0.223618	Magmas
2516	NM_013349.1	0.035714	0.035247	0.028748	0.223073	SPUF
2517	NM_000884.1	0.035714	0.035247	0.064347	0.222421	IMPDH2
2518	BG167570	0.035714	0.04225	0.108243	0.219652	DKFZp762N1910
2519	NM_004551.1	0.035714	0.00747	0.06025	0.217427	NDUFS3
2520	BG231932	0.035714	0.04225	0.079649	0.210447	CLN2
2521	NM_017851.1	0.035714	0.035247	0.036308	0.209956	FLJ20509
2522	NM_006519.1	0.035714	0.035247	0.032991	0.202387	TCTEL1
2523	AF032900.1	0.035714	0.035247	0.174549	0.200739	COQ7
2524	AL535380	0.035714	0.035247	0.265205	0.198073	BTG1
2525	AW118862	0.035714	0.035247	0.02173	0.193753	RREB1
2526	NM_000382.1	0.035714	0.035247	0.27948	0.193509	ALDH3A2
2527	NM_024419.1	0.035714	0.035247	0.164883	0.190623	PGS1
2528	NM_003904.1	0.035714	0.035247	0.245676	0.190422	ZNF259
2529	AI928526	0.035714	0.00747	0.036861	0.185624	JTV1

2530	NM_024581.1	0.035714	0.035247	0.230867	0.185323	FLJ13942
2531	AF085357.1	0.035714	0.035247	0.110175	0.184965	FLOT1
2532	NM_004475.1	0.035714	0.035247	0.072642	0.180483	FLOT2
2533	AF334103.1	0.035714	0.00747	0.009664	0.17511	GU2
2534	NM_017829.1	0.035714	0.035247	0.110207	0.174515	CECR5
2535	NM_004214.3	0.035714	0.04225	0.016835	0.157902	FIBP
2536	NM_017704.1	0.035714	0.04225	0.16159	0.157672	FLJ20189
2537	NM_003592.1	0.035714	0.035247	0.038652	0.146241	CUL1
2538	AI537887	0.035714	0.035247	0.467375	0.139355	EPB72
2539	NM_023935.1	0.035714	0.035247	0.049119	0.125305	C20orf116
2540	BG398414	0.035714	0.035247	0.286856	0.123085	RPA1
2541	NM_016243.1	0.035714	0.035247	0.279995	0.121894	LOC51706
2542	NM_012199.1	0.035714	0.035247	0.093241	0.118547	EIF2C1
2543	AK024029.1	0.035714	0.04225	0.450393	0.11646	MAP-1
2544	NM_004848.1	0.035714	0.035247	0.486492	0.113516	ICB-1
2545	AF144638.1	0.035714	0.035247	0.255571	0.10089	SGPL1
2546	D86062.1	0.035714	0.035247	0.532398	0.084417	C21orf33
2547	NM_000655.2	0.035714	0.035247	0.535745	0.081167	SELL
2548	NM_018643.1	0.035714	0.035247	0.870775	0.057399	TREM1
2549	NM_018326.1	0.035714	0.035247	0.929375	0.035048	HIMAP4
2550	NM_005371.2	0.035714	0.035247	0.876737	0.025127	METTL1
2551	NM_007002.1	0.035714	0.035247	0.911541	0.010422	ADRM1
2552	NM_004723.1	0.035714	0.035247	0.975685	-0.00562	ARHGEF2
2553	U31501	0.035714	0.035247	0.724549	-0.0658	FXR2
2554	NM_005338.3	0.035714	0.04225	0.126911	-0.0661	HIP1
2555	AB006589.1	0.035714	0.035247	0.00542	-0.10655	ESR2
2556	AA868754	0.035714	0.035247	0.304519	-0.10746	KIAA0650
2557	AU144792	0.035714	0.035247	0.008623	-0.11362	
2558	AF320999.1	0.035714	0.035247	0.289096	-0.11449	RTN4
2559	NM_013229.1	0.035714	0.035247	0.529181	-0.13735	APAF1
2560	NM_018690.1	0.035714	0.04225	0.261146	-0.14482	APOB48R
2561	D42055.1	0.035714	0.04225	0.007978	-0.14841	NEDD4
2562	BF968633	0.035714	0.035247	0.135003	-0.14873	RNF4
2563	AK026678.1	0.035714	0.035247	0.00833	-0.15056	STAG2
2564	NM_014671.1	0.035714	0.035247	0.392979	-0.15386	KIAA0010
2565	NM_030979.1	0.035714	0.035247	0.087494	-0.15652	PABPC3
2566	BG429214	0.035714	0.035247	0.273519	-0.15766	
2567	NM_006892.1	0.035714	0.035247	0.001922	-0.15828	DNMT3B
2568	NM_018975.1	0.035714	0.035247	0.042202	-0.16723	RAP1
2569	AL137335.1	0.035714	0.035247	0.306422	-0.17292	RANBP7
2570	NM_014016.1	0.035714	0.035247	0.398036	-0.17365	SACM1L
2571	NM_012198.1	0.035714	0.035247	0.391555	-0.17556	GCA
2572	NM_024586.1	0.035714	0.04225	0.011965	-0.19298	OSBPL9
2573	N64643	0.035714	0.035247	0.16498	-0.19313	KIAA0625
2574	NM_005951.1	0.035714	0.035247	0.156965	-0.1942	MT1H
2575	NM_002264.1	0.035714	0.035247	0.138195	-0.1949	

2576	AF182415.1	0.035714	0.04225	0.325959	-0.19495	RBM8A
2577	BE674061	0.035714	0.035247	0.015036	-0.20133	PIN4
2578	NM_004973.2	0.035714	0.00747	0.103071	-0.20162	JMJ
2579	U58852.1	0.035714	0.035247	0.510508	-0.20606	NPAT
2580	NM_005565.2	0.035714	0.035247	0.037541	-0.2105	LCP2
2581	NM_004941.1	0.035714	0.035247	0.229189	-0.21215	DDX8
2582	U02297.1	0.035714	0.035247	0.252672	-0.21782	SELPLG
2583	NM_002940.1	0.035714	0.035247	0.112373	-0.22731	ABCE1
2584	AL550657	0.035714	0.035247	0.069403	-0.23303	BSG
2585	BG387770	0.035714	0.035247	0.032984	-0.2362	MGC32104
2586	AL050205.1	0.035714	0.04225	0.352078	-0.23748	LOC113251
2587	NM_016653.1	0.035714	0.035247	0.003387	-0.23765	ZAK
2588	AA742237	0.035714	0.035247	0.120935	-0.23853	BAT2
2589	NM_021183.1	0.035714	0.035247	0.069121	-0.24239	LOC57826
2590	AB014527.1	0.035714	0.035247	0.005636	-0.24315	CLASP2
2591	AF091086.1	0.035714	0.035247	0.124853	-0.24621	CL640
2592	NM_006748.1	0.035714	0.04225	0.141473	-0.24728	SLA
2593	NM_025238.1	0.035714	0.035247	0.046507	-0.24841	BTBD1
2594	NM_018638.2	0.035714	0.035247	0.074405	-0.24942	EKI1
2595	NM_002913.1	0.035714	0.04225	0.092197	-0.24967	
2596	NM_002863.1	0.035714	0.035247	0.034567	-0.25494	PYGL
2597	AF226044.1	0.035714	0.035247	0.023966	-0.25679	SNRK
2598	NM_016217.1	0.035714	0.035247	0.01673	-0.25733	LOC51696
2599	AF084943.1	0.035714	0.035247	0.024841	-0.26011	MINPP1
2600	N22548	0.035714	0.04225	0.03686	-0.26164	ROCK1
2601	AF033850.1	0.035714	0.035247	0.110532	-0.26338	PLD2
2602	NM_014445.1	0.035714	0.00747	0.007058	-0.26858	SERP1
2603	NM_016196.1	0.035714	0.035247	0.014278	-0.27109	KIAA0682
2604	NM_012252.1	0.035714	0.035247	0.020625	-0.27124	TFEC
2605	W72082	0.035714	0.035247	0.180599	-0.27284	C1QR1
2606	NM_016166.1	0.035714	0.035247	0.071782	-0.27429	PIAS1
2607	NM_022470.1	0.035714	0.035247	0.072884	-0.27655	WIG1
2608	NM_030797.1	0.035714	0.035247	0.039197	-0.27728	DKFZP566A1524
2609	NM_002199.2	0.035714	0.035247	0.250656	-0.27789	IRF2
2610	BC003360.1	0.035714	0.035247	0.02171	-0.27851	DDX18
2611	NM_004504.2	0.035714	0.035247	0.020834	-0.27873	HRB
2612	NM_012072.2	0.035714	0.035247	0.118494	-0.27892	C1QR1
2613	NM_018230.1	0.035714	0.035247	0.071301	-0.28019	NUP133
2614	NM_002727.1	0.035714	0.04225	0.038559	-0.28438	PRG1
2615	BC005338.1	0.035714	0.035247	0.114062	-0.28524	CAPZA2
2616	U60521.1	0.035714	0.04225	0.066643	-0.29174	CASP9
2617	AW188198	0.035714	0.035247	0.005126	-0.29178	TNFAIP6
2618	BE908931	0.035714	0.035247	0.017009	-0.29572	
2619	U64661	0.035714	0.04225	0.030982	-0.29704	
2620	AL021395	0.035714	0.04225	0.02084	-0.29857	
2621	NM_015176.1	0.035714	0.035247	0.059688	-0.299	KIAA0483

2622	NM_002857.1	0.035714	0.04225	0.04761	-0.29944	PXF
2623	U70451.1	0.035714	0.035247	0.003458	-0.30169	MYD88
2624	NM_018042.1	0.035714	0.035247	0.020209	-0.30409	FLJ10260
2625	AL049265.1	0.035714	0.04225	0.136618	-0.30472	
2626	NM_024081.1	0.035714	0.035247	0.020267	-0.30513	TMG4
2627	AI796169	0.035714	0.035247	0.023959	-0.31104	GATA3
2628	AA160522	0.035714	0.035247	0.056044	-0.31114	UBE3A
2629	AL136621.1	0.035714	0.04225	0.06859	-0.31538	ZNF198
2630	NM_003051.1	0.035714	0.035247	0.028776	-0.3171	SLC16A1
2631	AW572909	0.035714	0.035247	0.027025	-0.31713	KIAA0874
2632	NM_017782.1	0.035714	0.04225	0.017104	-0.32078	FLJ20360
2633	AK001821.1	0.035714	0.04225	0.013182	-0.32145	MGC4170
2634	AW001847	0.035714	0.035247	0.204195	-0.32259	APLP2
2635	BF196931	0.035714	0.04225	0.003706	-0.3226	ZFP95
2636	AJ223333.1	0.035714	0.035247	0.023593	-0.32279	DNMT2
2637	NM_005213.1	0.035714	0.04225	0.216305	-0.32285	CSTA
2638	AF142419.1	0.035714	0.04225	0.013772	-0.33425	QKI
2639	NM_020375.1	0.035714	0.035247	0.07666	-0.33473	C12orf5
2640	NM_021970.1	0.035714	0.04225	0.054987	-0.33505	MAP2K1IP1
2641	AK023816.1	0.035714	0.035247	0.136952	-0.34214	
2642	NM_012238.3	0.035714	0.00747	0.018308	-0.3438	SIRT1
2643	AF205218.1	0.035714	0.035247	0.033088	-0.34674	NS1-BP
2644	NM_001660.2	0.035714	0.035247	0.020387	-0.35015	ARF4
2645	NM_001196.1	0.035714	0.015406	0.020544	-0.35511	BID
2646	NM_002970.1	0.035714	0.035247	0.064201	-0.35676	SAT
2647	AC074331	0.035714	0.035247	0.01515	-0.35767	
2648	M75715.1	0.035714	0.035247	0.010802	-0.3577	ETF1
2649	NM_018657.2	0.035714	0.04225	0.021807	-0.3681	MYNN
2650	NM_003370.1	0.035714	0.035247	0.056143	-0.37617	VASP
2651	AI761561	0.035714	0.035247	0.084393	-0.37861	HK2
2652	NM_002657.2	0.035714	0.035247	0.043402	-0.39004	PLAGL2
2653	NM_004565.1	0.035714	0.035247	0.086212	-0.39025	PEX14
2654	AK023837.1	0.035714	0.04225	0.083366	-0.39056	KIAA1025
2655	AL117354	0.035714	0.00747	0.011916	-0.39754	LOC50999
2656	NM_001356.2	0.035714	0.035247	0.029134	-0.41337	DDX3
2657	NM_018573.1	0.035714	0.015406	0.00529	-0.41757	PRO1068
2658	NM_030799.1	0.035714	0.035247	0.075235	-0.42088	SMAP-5
2659	AA524053	0.035714	0.04225	0.031361	-0.42442	
2660	NM_002748.1	0.035714	0.035247	0.023266	-0.42563	MAPK6
2661	NM_002053.1	0.035714	0.035247	0.053201	-0.43747	GBP1
2662	AB023227.1	0.035714	0.04225	0.003343	-0.43985	KIAA1010
2663	AW193511	0.035714	0.035247	0.012709	-0.44652	HIS1
2664	AW272611	0.035714	0.04225	0.024277	-0.44899	TMPO
2665	AI671747	0.035714	0.00747	0.02288	-0.45263	MISS
2666	AI688580	0.035714	0.035247	0.035918	-0.45484	SURB7
2667	NM_002502.1	0.035714	0.035247	0.107712	-0.45745	NFKB2

2668	NM_004267.1	0.035714	0.04225	0.030352	-0.47177	CHST2
2669	X15132.1	0.035714	0.035247	0.041452	-0.47259	SOD2
2670	NM_012093.1	0.035714	0.035247	0.011606	-0.47474	AK5
2671	D26067.1	0.035714	0.035247	0.003438	-0.47644	KIAA0033
2672	NM_001166.2	0.035714	0.04225	0.015252	-0.48334	BIRC2
2673	NM_016545.1	0.035714	0.035247	0.029826	-0.48723	IER5
2674	NM_021122.2	0.035714	0.035247	0.070882	-0.49855	FACL2
2675	NM_017936.1	0.035714	0.035247	0.008293	-0.5016	FLJ20707
2676	NM_000574.1	0.035714	0.035247	0.022743	-0.50532	DAF
2677	AL050144.1	0.035714	0.015406	0.000822	-0.52839	ZNF363
2678	NM_005346.2	0.035714	0.035247	0.10824	-0.5359	HSPA1B
2679	NM_022725.1	0.035714	0.035247	0.023814	-0.53779	FANCF
2680	AI348010	0.035714	0.035247	0.226116	-0.54348	
2681	AI927993	0.035714	0.035247	0.054067	-0.54478	OSBP
2682	BE327172	0.035714	0.035247	0.091317	-0.54925	JUN
2683	AI741876	0.035714	0.00747	0.025182	-0.57505	
2684	NM_003107.1	0.035714	0.035247	0.078087	-0.59709	SOX4
2685	BE383139	0.035714	0.035247	0.00951	-0.60058	RARA
2686	NM_018398.1	0.035714	0.035247	0.016221	-0.603	CACNA2D3
2687	NM_000201.1	0.035714	0.035247	0.036915	-0.62554	ICAM1
2688	NM_002229.1	0.035714	0.035247	0.129802	-0.64436	JUNB
2689	NM_021960.1	0.035714	0.04225	0.024176	-0.66914	MCL1
2690	NM_016010.1	0.035714	0.00747	0.015684	-0.68307	LOC51101
2691	NM_004417.2	0.035714	0.035247	0.043377	-0.68458	DUSP1
2692	NM_025195.1	0.035714	0.035247	0.055882	-0.68638	C8FW
2693	NM_004418.2	0.035714	0.035247	0.306591	-0.68934	DUSP2
2694	AB017493.1	0.035714	0.015406	0.010224	-0.6982	COPEB
2695	AF064824.1	0.035714	0.035247	0.010071	-0.70109	RIPK2
2696	NM_005354.2	0.035714	0.035247	0.04394	-0.70667	JUND
2697	NM_006469.1	0.035714	0.035247	0.006453	-0.71493	NS1-BP
2698	NM_006290.1	0.035714	0.035247	0.155375	-0.73437	TNFAIP3
2699	AI339541	0.035714	0.035247	0.039838	-0.76402	JUND
2700	AF087853.1	0.035714	0.035247	0.076647	-0.77217	GADD45B
2701	AL031602	0.035714	0.035247	0.015158	-0.78504	
2702	BF575213	0.035714	0.035247	0.007144	-0.78651	
2703	M68956.1	0.035714	0.00747	0.001933	-0.79718	MARCKS
2704	NM_004907.1	0.035714	0.035247	0.006503	-0.81053	ETR101
2705	AW083357	0.035714	0.035247	0.009893	-0.81405	IL1RN
2706	AF153820.1	0.035714	0.035247	0.004403	-0.82757	KCNJ2
2707	AI608725	0.035714	0.035247	0.010119	-0.83319	ICAM1
2708	NM_000958.1	0.035714	0.015406	0.003112	-0.86354	PTGER4
2709	AA083483	0.035714	0.035247	0.012228	-0.88452	FTH1
2710	NM_002664.1	0.035714	0.00747	0.000855	-0.88664	PLEK
2711	AL031602	0.035714	0.015406	0.00038	-0.88673	
2712	W27419	0.035714	0.015406	0.000361	-0.95575	
2713	NM_002852.1	0.035714	0.035247	0.001716	-0.97365	PTX3

2714	NM_001964.1	0.035714	0.035247	0.068287	-0.99045	EGR1
2715	AF078077.1	0.035714	0.035247	0.017058	-1.003	GADD45B
2716	NM_015714.1	0.035714	0.035247	0.210858	-1.05996	G0S2
2717	BC004490.1	0.035714	0.035247	0.068201	-1.06388	FOS
2718	AI738896	0.035714	0.035247	0.071526	-1.09453	TNFAIP3
2719	AW973834	0.035714	0.035247	0.030817	-1.09468	
2720	NM_004895.1	0.035714	0.035247	0.004992	-1.10724	CIAS1
2721	U08839.1	0.035714	0.035247	0.030968	-1.1245	PLAUR
2722	BC005020.1	0.035714	0.035247	0.022893	-1.13801	PPIF
2723	NM_005627.1	0.035714	0.035247	0.010834	-1.16132	SGK
2724	NM_015675.1	0.035714	0.035247	0.022251	-1.16822	GADD45B
2725	AI433595	0.035714	0.015406	0.002395	-1.17663	PLEK
2726	NM_002135.1	0.035714	0.035247	0.009942	-1.19934	NR4A1
2727	NM_003407.1	0.035714	0.035247	0.0028	-1.30448	ZFP36
2728	NM_004233.1	0.035714	0.035247	0.045128	-1.33091	CD83
2729	NM_001432.1	0.035714	0.035247	0.001942	-1.33633	EREG
2730	NM_002228.2	0.035714	0.035247	0.007227	-1.34352	JUN
2731	NM_004049.1	0.035714	0.035247	0.004927	-1.41895	BCL2A1
2732	U83981	0.035714	0.035247	0.005806	-1.46885	PPP1R15A
2733	NM_006018.1	0.035714	0.035247	0.002094	-1.50671	HM74
2734	BG491844	0.035714	0.035247	0.011957	-1.61438	JUN
2735	BC002646.1	0.035714	0.035247	0.002438	-1.64136	JUN
2736	NM_000963.1	0.035714	0.035247	0.025772	-1.65759	PTGS2
2737	AY029180.1	0.035714	0.035247	0.011082	-1.69399	PLAUR
2738	NM_014330.2	0.035714	0.035247	0.003245	-1.74665	PPP1R15A
2739	NM_003897.1	0.035714	0.035247	0.002981	-1.89968	IER3
2740	M57731.1	0.035714	0.035247	0.001811	-1.9703	CXCL2
2741	NM_000584.1	0.035714	0.035247	0.030747	-2.54298	IL8
2742	NM_000576.1	0.035714	0.035247	0.000992	-2.66025	IL1B
2743	M15330	0.035714	0.035247	0.001505	-2.71142	IL1B

It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable subcombination.

Although the invention has been described in conjunction with specific embodiments thereof, it is evident that many alternatives, modifications and

variations will be apparent to those skilled in the art. Accordingly, it is intended to embrace all such alternatives, modifications and variations that fall within the spirit and broad scope of the appended claims. All publications, patents, patent applications and sequences identifies by a GenBank accession number mentioned in this specification are herein incorporated in their entirety by reference into the specification, to the same extent as if each individual publication, patent, patent application or sequence was specifically and individually indicated to be incorporated herein by reference. In addition, citation or identification of any reference in this application shall not be construed as an admission that such reference is available as prior art to the present invention.